
W P E R L H (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 25 12:25:47 2000; MasPar time 23.67 Seconds
Tabular output not generated. 26.013 Million cell updates/sec

Title: >seqmod
Description: (1-26) from 103.pap
Perfect Score: 140
Sequence: 1 ISTXSLSLDIALXXXLPXMRIVEIY 26

Scoring table: PAM 150
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq36
l:geneseqp

Statistics: Mean 20.429; Variance 79.314; scale 0.258

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	140	100.0	358	1	Hyperrecombinogenic va	5.62e-06
2	140	100.0	358	1	New minshall reca prot	5.62e-06
3	140	100.0	358	1	Hyperrecombinogenic va	5.62e-06
4	140	100.0	358	1	Hyperrecombinogenic va	5.62e-06
5	140	100.0	358	1	Hyperrecombinogenic va	5.62e-06
6	140	100.0	358	1	Hyperrecombinogenic va	5.62e-06
7	123	87.9	348	1	Reca gene product.	2.63e-04
8	113	80.7	273	1	Deduced sequence of re	2.43e-03
9	113	80.7	273	1	Helicobacter pylori re	2.43e-03
10	113	80.7	347	1	Helicobacter pylori re	2.43e-03
11	99	70.7	344	1	Reca.	5.22e-02
12	97	69.3	340	1	Thermus aquaticus RecA	8.03e-02
13	94	67.1	338	1	B. flavum MJ-233 RecA	1.53e-01
14	90	64.3	438	1	Arabidopsis thaliana R	3.59e-01
15	72	51.4	389	1	Rice protein from a ge	1.51e+01
16	65	46.4	453	1	T-cell transmembra	6.08e+01
17	65	46.4	453	1	T-cell transmembra	6.08e+01
18	65	46.4	453	1	T-cell transmembra	6.08e+01
19	63	45.0	622	1	Human T-cell early act	8.99e+01
20	63	45.0	622	1	ERR receptor.	8.99e+01
21	63	45.0	707	1	Murine ecotropic retro	8.99e+01
22	62	44.3	367	1	ApXIB protein.	1.09e+02
23	62	44.3	367	1	Partial human H13 poly	1.09e+02
					Human retroviral recep	1.09e+02

24	62	44.3	628	1	R54876	Human H13 viral recept	1.09e+02
25	62	44.3	628	1	R54872	Human H13 viral recept	1.09e+02
26	62	44.3	629	1	R25072	H13 gene product.	1.09e+02
27	62	44.3	629	1	R54868	Full-length human H13	1.09e+02
28	62	44.3	629	1	R54870	Human H13 viral recept	1.09e+02
29	62	44.3	629	1	R54871	Human H13 viral recept	1.09e+02
30	62	44.3	629	1	W67473	Human retroviral recep	1.09e+02
31	62	44.3	629	1	R54875	Human H13 viral recept	1.09e+02
32	62	44.3	629	1	R54873	Human H13 viral recept	1.09e+02
33	62	44.3	629	1	R54874	Human H13 viral recept	1.09e+02
34	62	44.3	629	1	R54869	Human H13 viral recept	1.09e+02
35	62	44.3	629	1	R47121	Full-length human H13	1.09e+02
36	62	44.3	1500	1	R30636	hCPSI.	1.09e+02
37	61	43.6	709	1	W33345	Human adenylyl cyclase	1.32e+02
38	61	43.6	1288	1	W61369	Rat 5-oxoprolinase.	1.32e+02
39	61	43.6	2386	1	W13153	S. pombe Rad3 polypept	1.32e+02
40	60	42.9	217	1	W34132	Streptococcus pneumoni	1.61e+02
41	60	42.9	217	1	W83376	Streptococcus pneumoni	1.61e+02
42	59	42.1	41	1	R25796	[Ala13]-Arg23-alpha-he	1.94e+02
43	59	42.1	379	1	W26368	Human kidney inward re	1.94e+02
44	59	42.1	514	1	R95044	Apoptosis participation	1.94e+02
45	59	42.1	1594	1	P81184	Sequence encoded by th	1.94e+02

ALIGNMENTS

RESULT 1
ID W64214 standard; Protein; 358 AA.
AC W64214;

DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant reca protein clone 2.
KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.

OS Synthetic.
PN WO9831837-A1.

PD 23-JUL-1998.
PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.

PI Deicardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;

DR WPI; 98-427565/36.
DR N-PSDB; V44286.

PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function

PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g. for
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC reca protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
||| ||||| ||| |||||

QY 1 ISTXSLSLDIALXXXLPXMRIVEIY 26

RESULT 2
ID W64213 standard; Protein; 358 AA.

AC W64213;
DT 28-APR-1999 (first entry)

DE New minshall reca protein.
KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.

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OS Escherichia coli.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44285.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a wild-type recA protein (designated
CC new Minshall), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEYIY 26

RESULT 3
ID W64216 standard; Protein: 358 AA.
AC W64216;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 5.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44288.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEYIY 26

RESULT 4
ID W64218 standard; Protein: 358 AA.
AC W64218;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 13.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44290.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEYIY 26

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ID W64215 standard; Protein: 358 AA.
AC W64215;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 4.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44287.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
   ||| ||||| ||| |||||
QY 1 ISTXSLSLDIALXXXXLPMXRIEYIY 26

RESULT 5
ID W64218 standard; Protein: 358 AA.
AC W64218;
DT 28-APR-1999 (first entry)
DE Hyperrecombinogenic variant recA protein clone 13.
KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
KW recursive sequence recombination; evolution.
OS Escherichia coli.
OS Synthetic.
PN WO9831837-Al.
PD 23-JUL-1998.
PF 16-JAN-1998; U00852.
PR 17-JAN-1997; US-035054.
PA (MAXY-) MAXYGEN INC.
PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,
PI Tobin MB;
DR N-PSDB; V44290.
DR WPI; 98-427565/36.
PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function
PS Example 1; Fig 13; 125pp; English.
CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombination, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 5.62e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 46 ISTGSLSLDIALGAGGLPMGRIVEY 71
 ||| ||||| ||| |||||
 QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 6
 ID W64217 standard; Protein; 358 AA.
 AC W64217;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 6.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 NC Synthetic.
 WO9831837-A1.
 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB;
 DR WPI; 98-427565/36.
 DR N-PSDB; V44289.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see W64213), from an example of the present invention.
 SQ Sequence 358 AA;

Query Match 100.0%; Score 140; DB 1; Length 358;
 Best Local Similarity 76.9%; Pred. No. 5,62e-06; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 6;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEY 71
 ||| ||||| ||| |||||
 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 7
 ID R40973 standard; Protein; 348 AA.
 AC R40973;
 DT 04-MAR-1994 (first entry)
 DE recA gene product.
 KW recA; microbe; acetic acid bacterium.
 OS Acetobacter altoacetigenes.
 PN J0519987-A.
 PD 10-AUG-1993.
 PF 30-JAN-1991; 094678.
 PR 09-FEB-1990; JP-028391.
 PA (NAKA-) NAKANO SUTEN KK.
 DR WPI; 93-284684/36.
 DR N-PSDB; Q48658.
 PT Acetic acid bacterium recA gene - with plasmid contg. it and a
 PT transformed acetic acid bacterium
 PS Claim 1; Page 8-10; 10pp; Japanese.
 CC The recA gene can control the recombination activity of the
 CC acetic acid bacterium gene.
 SQ Sequence 348 AA;

Query Match 87.9%; Score 123; DB 1; Length 348;
 Best Local Similarity 65.4%; Pred. No. 2.63e-04; Indels 0; Gaps 0;
 Matches 17; Conservative 2; Mismatches 7;

Db 43 ISTGSLSLDIALGGLPRGRIVEY 68
 ||| ||||| ||| |||||

QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 8
 ID R79145 standard; Protein; 273 AA.
 AC R79145;
 DT 28-DEC-1995 (first entry)
 DE Deduced sequence of recombinase encoded by H. pylori RecA gene.
 KW Recombinase; recA; Helicobacter pylori.
 OS Helicobacter pylori.
 FH Key Location/Qualifiers
 FT misc_difference 67
 FT /label= conserved in bacterial RecA proteins
 FT misc_difference 73.74
 FT /label= see above
 FT misc_difference 95
 FT /label= see above
 FT misc_difference 97
 FT /label= see above
 FT misc_difference 104
 FT /label= see above
 FT misc_difference 145.146
 FT /label= see above
 FT misc_difference 194.195
 FT /label= see above
 FT misc_difference 213
 FT /label= see above

US5434253-A.
 PN 18-JUL-1995.
 PD 21-MAR-1994; 215928.
 PR 21-MAR-1994; US-215928.
 PA (UYVA-) UNIV VANDERBILT.
 PI Blaser MJ, Thompson SA;
 DR WPI; 95-263283/34.
 DR N-PSDB; Q96252.
 PT Nucleic acid encoding a portion of Helicobacter pylori recombinase
 PT used e.g. for detecting H. pylori or producing recombinant enzyme.
 PS Disclosure; Columns 13-16; 14pp; English.
 CC A genomic library was prepd. in lambdaZAPII from partially
 CC Alu-digested H. pylori 84-183 chromosomal DNA. The PCR-amplified
 CC recA fragment (see Q96253) was used as probe and identified 3
 CC identical clones contg. 2.3 kb inserts. One of these was designated
 CC pSAT101 (Q96251). The deduced AA sequence (R79145) of this ORF
 CC showed high similarity to bacterial RecA proteins when used in
 CC a BLAST search of GenBank. The ORF contd. on pSAT101 does not
 CC contain a termination codon. This ORF, therefore, is approx.
 CC 80% the length of a typical bacterial recA gene. All of the
 CC highly conserved or invariant residues in bacterial RecA proteins
 CC and related bacteriophage and yeast proteins are present and in
 CC the predicted location in the deduced AA sequence of the pSAT101
 CC ORF.
 SQ Sequence 273 AA;

Query Match 80.7%; Score 113; DB 1; Length 273;
 Best Local Similarity 57.7%; Pred. No. 2.43e-03; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Mismatches 6;

Db 41 ISTGSLSLDIALGIGVPGRIIIEY 66
 ||| ||||| ||| |||||
 QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 9
 ID W44140 standard; Protein; 273 AA.
 AC W44140;
 DT 05-MAY-1998 (first entry)
 DE Helicobacter pylori recombinase fragment encoded from pSAT101.
 KW Helicobacter pylori; recombinase; enolase; mutant; strain;
 KW nonfunctional.
 OS Helicobacter pylori.
 PN US5703219-A.
 PD 30-DEC-1997.
 PF 22-MAY-1995; 446920;

RESULT	11
ID	R15141 standard; Protein; 344 AA.
AC	R15141.
DT	24-FEB-1992 (first entry)
DE	RecA.
KW	Recombinant repair; amplification.
OS	Escherichia coli magnetotacticum.
EN	W09117267-A.
PD	14-NOV-1991.
PF	17-APR-1991; U02626.
PR	07-MAY-1990; U520321.

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Db      39 IPTGSLGLDALGIGGIPRGRVTEIF 64  
          | : | | | | | | | : | : | | :  
Qv      1 ISTXSLSDIALXXXXLPMXRIVEIY 26
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RESULT 13
ID R90681 standard; Protein; 338 AA.
AC R90681;
DT 11-JUL-1996 (first entry)
DE B. flavum MJ-233 RecA protein.
KW RecA protein; gene recombination; increase; transformant;
OS transformed; activity; Corynebacterium.
PN J07322879-A.
PD 12-DEC-1995.
PF 30-MAY-1994; 116589.
PR 30-MAY-1994; JP-116689.
RA (MITU) MITSUBISHI CHEM CORP.
PA WPI: 96-064845/07.
N-PSDB; T15532.
PT DNA fragment contg. gene encoding RecA protein from Brevibacterium
PS flavum - useful for increasing gene recombination in bacteria
PS Claim 4; Pages 8-9; 9pp; Japanese.
CC The present sequence is the B. flavum MJ-233 RecA protein,
CC which can be used to increase gene recombination in bacteria, i.e.
CC a transformant transformed with the recA gene has an improved gene
CC recombination activity.
SQ Sequence 338 AA.

Query Match 67.1%; Score 94; DB 1; Length 338;
Best Local Similarity 46.2%; Pred. No. 1.53e-01;
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 14 ISSGNTAIDALGIGGFGPRIVEY 39
QY 1 ISTXSLDLALXXXLPMXRIVEY 26

RESULT 14
ID W34658 standard; Protein; 438 AA.
AC W34658;
DT 13-FEB-1998 (first entry)
DE Arabidopsis thaliana Rec-A protein.
KW Rec-A protein; Synchococcus recA gene; transit peptide;
KW homologous recombination; DNA repair; the recA gene.
OS Arabidopsis thaliana.
PA Cerutti H. Jagendorf A;
PI WPI: 97-502391/46.
N-PSDB; T93777.
PT DNA encoding chloroplast RecA-like protein from Arabidopsis thaliana
PT - useful for increasing the frequency of homologous chromosomal
PT recombination when lacking the transit peptide sequence
PS Claim 2; Columns 7-9; 14pp; English.
CC The present sequence is of a Rec-A like protein from Arabidopsis
CC thaliana. The cDNA encoding this protein (T93777) was isolated from an
CC Arabidopsis library screened with a Synchococcus recA gene. The cDNA
CC sequence is truncated at its 5' end, and the start of the open reading
CC frame, and thus the start of the transit peptide, is missing. In E. coli,
CC and many other prokaryotes, the Rec-A protein is essential for homologous
CC recombination, and DNA repair. In view of this role, it is likely that
CC that the enzyme encoded by the present sequence may also be concerned
CC with DNA repair. The 5' end of the recA gene, i.e. the portion encoding
CC the transit peptide part of the protein that directs the final product
CC into chloroplast, could be removed and replaced by an amino acid sequence
CC that directs completed proteins to enter the nucleus. By introducing the

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CC RecA protein into the nuclei of higher plants, it should be possible to
CC increase the frequency of homologous recombination in the chromosomal
CC genes of the plants.
SQ Sequence 438 AA;

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Query Match 64.3%; Score 90; DB 1; Length 438;
Best Local Similarity 50.0%; Pred. No. 3.59e-01;
Matches 13; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

Db 116 FSSGILDLALGGG-LPKGRVVEY 140
QY 1 ISTXSLDLALXXXLPMXRIVEY 26

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RESULT 15
ID W16842 standard; Protein; 389 AA.
AC W16842;
DT 23-MAR-1998 (first entry)
DE Rice protein from a gene expressed at the mono-nuclear anther stage.
KW Rice; mono-nuclear anther stage; expression; screening; cDNA library.
OS Oryza sativa.
PN J09075091-A.
PD 25-MAR-1997.
PF 13-SEP-1995; 273368.
PR 13-SEP-1995; JP-273368.
PA (IWAT-) IWATE KEN.
DR WPI: 97-239273/22.
DR N-PSDB; T66892.
PT Rice genes specifically expressed at the mono-nuclear stage of
PT anther - useful for screening cDNA libraries for other anther genes
PS Claim 4; Page 7-10; 10pp; Japanese.
CC The present sequence represents a rice (Oryza sativa) protein from a
CC gene which is expressed at the mono-nuclear anther stage. The gene can
CC be used for screening cDNA libraries for other Oryza sativa anther
CC genes. The sequences can also be used to produce Oryza sativa with
CC favourable characteristic features.
SQ Sequence 389 AA;

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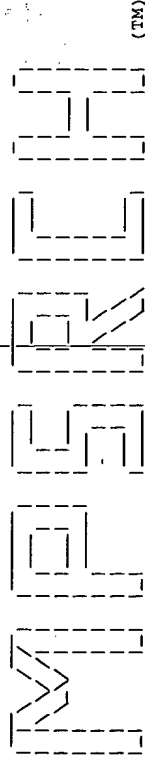
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Query Match 51.4%; Score 72; DB 1; Length 389;
Best Local Similarity 38.1%; Pred. No. 1.51e+01;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Db 27 LALGKGLPEQVLPOEKVVVEY 47
QY 6 LSLDLALXXXLPMXRIVEY 26

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Search completed: Tue Apr 25 12:26:29 2000
Job time : 42 secs.



 (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Apr 25 12:30:48 2000; MasPar time 14.95 Seconds
 Tabular output not generated. 191.070 Million cell updates/sec

Title: >seqmod
 Description: (1-26) from 103.pap
 Perfect Score: 140
 Sequence: 1 ISYXSLSLDIALXXXLPMXRIIVEIY 26

Scoring table: PAM 150
 Gap 15

Searched: 702510 seqs, 109899995 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-pending
 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84A 9:U84B
 10:U85 11:U86 12:U87 13:U88 14:U89 15:U90 16:U91 17:U92
 18:U93 19:U94 20:NEWP 21:NEWU60 22:NEWU6 23:NEWU7
 24:NEWU8 25:NEWU9

Statistics: Mean 23.645; Variance 78.234; scale 0.302

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Description	Pred. No.
1	140	100.0	Sequence 1, Applicatio	3.58e-06
2	140	100.0	Sequence 9, Applicatio	3.58e-06
3	140	100.0	Sequence 10, Applicati	3.58e-06
4	140	100.0	Sequence 11, Applicati	3.58e-06
5	140	100.0	Sequence 8, Applicatio	3.58e-06
6	140	100.0	Sequence 13, Applicati	3.58e-06
7	140	100.0	Sequence 15, Applicati	3.58e-06
8	140	100.0	Sequence 17, Applicati	3.58e-06
9	126	90.0	Sequence 12, Applicati	1.31e-04
10	124	88.6	Sequence 7563, Applic	2.18e-04
11	120	85.7	Sequence 14, Applicati	6.02e-04
12	120	85.7	Sequence 6, Applicatio	6.02e-04
13	118	84.3	Sequence 4548, Applic	9.97e-04
14	115	82.1	Sequence 4, Applicatio	2.12e-03
15	115	82.1	Sequence 2, Applicatio	2.12e-03
16	115	82.1	Sequence 8, Applicatio	2.12e-03
17	115	82.1	Sequence 8, Applicatio	2.12e-03
18	115	80.7	Sequence 7471, Applic	3.49e-03
19	113	80.7	Sequence 2, Applicatio	3.49e-03
20	113	80.7	Sequence 7472, Applic	3.49e-03

21	113	80.7	347 13	US-08-892-	Sequence 230, Applicat	3.49e-03
22	113	80.7	347 14	US-08-993-	Sequence 7473, Applic	3.49e-03
23	113	80.7	409 18	US-09-310-	Sequence 4, Applicatio	3.49e-03
24	108	77.1	430 18	US-09-310-	Sequence 6, Applicatio	1.21e-02
25	108	77.1	430 18	US-09-310-	Sequence 6, Applicatio	1.21e-02
26	102	72.9	380 20	PCT-US99-2	Sequence 764, Applicat	5.28e-02
27	99	70.7	147 18	US-09-370-	Sequence 4, Applicatio	1.10e-01
28	90	64.3	438 3	US-07-938-	Sequence 2, Applicatio	9.49e-01
29	86	61.4	384 18	US-09-310-	Sequence 2, Applicatio	2.43e+00
30	86	61.4	384 18	US-09-310-	Sequence 2, Applicatio	2.43e+00
31	85	60.7	26 25	US-09-358-	Sequence 3, Applicatio	3.07e+00
32	81	57.9	357 19	US-09-450-	Sequence 4382, Applic	7.77e+00
33	79	56.4	314 16	US-09-134-	Sequence 3591, Applic	1.23e+01
34	72	51.4	360 25	US-09-340-	Sequence 7, Applicatio	5.93e+01
35	70	50.0	603 19	US-09-417-	Sequence 40324, Applic	9.22e+01
36	69	49.3	575 16	US-09-107-	Sequence 3910, Applic	1.15e+02
37	65	46.4	192 25	US-09-497-	Sequence 606, Applicat	2.72e+02
38	65	46.4	242 16	US-09-107-	Sequence 3774, Applic	2.72e+02
39	65	46.4	347 2	US-60-167-	Sequence 16795, Applic	2.72e+02
40	65	46.4	347 2	US-60-164-	Sequence 16071, Applic	2.72e+02
41	65	46.4	560 4	US-08-074-	Sequence 4, Applicatio	2.72e+02
42	65	46.4	1088 2	US-60-173-	Sequence 23774, Applic	2.72e+02
43	65	46.4	1088 2	US-60-173-	Sequence 30577, Applic	2.72e+02
44	65	46.4	1157 2	US-60-164-	Sequence 18095, Applic	2.72e+02
45	65	46.4	3921 7	US-08-396-	Sequence 2, Applicatio	2.72e+02

ALIGNMENTS

RESULT 1
 ID US-09-358-103-1 STANDARD; PRT; 26 AA.

XX xxxxxx

Sequence 1, Application US/09358103B

Sequence 1, Application US/09358103B

GENERAL INFORMATION:

APPLICANT: Rocca, Alberto I

TITLE OF INVENTION: Mutants of MAW Motifs of RecA Protein Homologs, Methods of Making Them, and Their Uses

FILE REFERENCE: RecA Homolog Protein & Mutants

CURRENT APPLICATION NUMBER: US/09/358,103B

CURRENT FILING DATE: 1993-07-21

EARLIER APPLICATION NUMBER: 60/094,071

EARLIER FILING DATE: 1998-07-24

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 26

TYPE: PRT

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: NON_TER

LOCATION: (1)

FEATURE:

NAME/KEY: NON_TER

LOCATION: (26)..)

FEATURE:

NAME/KEY: HELIX

LOCATION: (6)..(12)

OTHER INFORMATION: Alpha-helix B

FEATURE:

NAME/KEY: STRAND

LOCATION: (22)..(26)

OTHER INFORMATION: Beta-strand 1

FEATURE:

NAME/KEY: SIMILAR

LOCATION: (1)..(26)

OTHER INFORMATION: This structure is highly conserved across bacterial RecA and homologous eukaryotic,

CC OTHER INFORMATION: archaeal, and viral proteins; sequence below is
CC OTHER INFORMATION: from E. coli RecA positions 40-65
SQ SEQUENCE 26 AA; 2604 MW; 3614 CN;

Query Match 100.0%; Score 140; DB 25; Length 26;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 1 ISTGSLSLDIALGAGGLPMGRIVEIY 26
||| ||||||| ||| |||||||
QY 1 ISTXSLSLDIALXXXXXLPXMRIVEIY 26

RESULT 2
ID US-09-354-922-9 STANDARD; PRT; 358 AA.

XX AC xxxxxx

Sequence 9, Application US/09354922

Sequence 9, Application US/09354922

GENERAL INFORMATION:
CC APPLICANT: DEL CARDAYRE, STEPHEN
CC APPLICANT: TOBIN, MATTHEW
CC APPLICANT: NISS, JON E.
CC APPLICANT: MINSHULL, JEREMY
CC APPLICANT: PATTEN, PHILLIP
CC APPLICANT: SUBRAMANIAN, VENKITESWATAN
CC APPLICANT: CASTLE, LINDA A.
CC APPLICANT: KREBER, CLAUD M.
CC APPLICANT: BASS, STEVE
CC APPLICANT: ZHANG, YING-XIN
CC APPLICANT: COX, TONY
CC APPLICANT: HUISMAN, GJALT
CC APPLICANT: YUAN, LING
CC APPLICANT: AFFHOLTER, JOSEPH A.
CC TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
CC TITLE OF INVENTION: SEQUENCE RECOMBINATION
CC FILE REFERENCE: 02-020730US
CC CURRENT APPLICATION NUMBER: US/09/354,922
CC CURRENT FILING DATE: 1999-07-15
CC NUMBER OF SEQ ID NOS: 15
CC SOFTWARE: PatentIn Ver. 2.0
CC SEQ ID NO 9
CC LENGTH: 358
CC TYPE: PRT
CC ORGANISM: Escherichia coli
CC SEQUENCE 358 AA; 38464 MW; 626707 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
||| ||||||| ||| |||||||
QY 1 ISTXSLSLDIALXXXXXLPXMRIVEIY 26

RESULT 3
ID US-09-354-922-10 STANDARD; PRT; 358 AA.

XX AC xxxxxx

Sequence 10, Application US/09354922

Sequence 10, Application US/09354922
GENERAL INFORMATION:
CC APPLICANT: DEL CARDAYRE, STEPHEN

CC APPLICANT: TOBIN, MATTHEW
CC APPLICANT: STEMMER, WILLEM P.C.
CC APPLICANT: NISS, JON E.
CC APPLICANT: MINSHULL, JEREMY
CC APPLICANT: PATTEN, PHILLIP
CC APPLICANT: SUBRAMANIAN, VENKITESWATAN
CC APPLICANT: CASTLE, LINDA A.
CC APPLICANT: KREBER, CLAUD M.
CC APPLICANT: BASS, STEVE
CC APPLICANT: ZHANG, YING-XIN
CC APPLICANT: COX, TONY
CC APPLICANT: HUISMAN, GJALT
CC APPLICANT: YUAN, LING
CC APPLICANT: AFFHOLTER, JOSEPH A.
CC TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
CC TITLE OF INVENTION: SEQUENCE RECOMBINATION
CC FILE REFERENCE: 02-020730US
CC CURRENT APPLICATION NUMBER: US/09/354,922
CC CURRENT FILING DATE: 1999-07-15
CC NUMBER OF SEQ ID NOS: 15
CC SOFTWARE: PatentIn Ver. 2.0
CC SEQ ID NO 10
CC LENGTH: 358
CC TYPE: PRT
CC ORGANISM: Escherichia coli
CC SEQUENCE 358 AA; 38404 MW; 628187 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLSLDIALGAGGLPMGRIVEIY 71
||| ||||||| ||| |||||||
QY 1 ISTXSLSLDIALXXXXXLPXMRIVEIY 26

RESULT 4
ID US-09-354-922-11 STANDARD; PRT; 358 AA.

XX AC xxxxxx

Sequence 11, Application US/09354922

Sequence 11, Application US/09354922
GENERAL INFORMATION:
CC APPLICANT: DEL CARDAYRE, STEPHEN
CC APPLICANT: TOBIN, MATTHEW
CC APPLICANT: NISS, JON E.
CC APPLICANT: MINSHULL, JEREMY
CC APPLICANT: PATTEN, PHILLIP
CC APPLICANT: SUBRAMANIAN, VENKITESWATAN
CC APPLICANT: CASTLE, LINDA A.
CC APPLICANT: KREBER, CLAUD M.
CC APPLICANT: BASS, STEVE
CC APPLICANT: ZHANG, YING-XIN
CC APPLICANT: COX, TONY
CC APPLICANT: HUISMAN, GJALT
CC APPLICANT: YUAN, LING
CC APPLICANT: AFFHOLTER, JOSEPH A.
CC TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE
CC TITLE OF INVENTION: SEQUENCE RECOMBINATION
CC FILE REFERENCE: 02-020730US
CC CURRENT APPLICATION NUMBER: US/09/354,922
CC CURRENT FILING DATE: 1999-07-15
CC NUMBER OF SEQ ID NOS: 15
CC SOFTWARE: PatentIn Ver. 2.0
CC SEQ ID NO 11
CC LENGTH: 358
CC TYPE: PRT
CC ORGANISM: Escherichia coli

OTHER INFORMATION: Description of Artificial Sequence: consensus

CC OTHER INFORMATION: e. coli sequence
SQ SEQUENCE 358 AA; 38490 MW; 627879 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLDIALGAGGLPMGRIVEY 71
||| ||||| ||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 8
ID US-09-354-922-12 STANDARD; PRT; 358 AA.

XX AC xxxxxx

Sequence 12, Application US/09354922

GENERAL INFORMATION:

APPLICANT: DEL CARDAYRE, STEPHEN

APPLICANT: TOBIN, MATTHEW

APPLICANT: STEMMER, WILLEM P.C.

APPLICANT: NESS, JON E.

APPLICANT: MINSHULL, JEREMY

APPLICANT: PATTEN, PHILLIP

APPLICANT: SUBRAMANIAN, VENKITESWATAN

APPLICANT: CASTLE, LINDA A.

APPLICANT: KREBER, CLAUS M.

APPLICANT: BASS, STEVE

APPLICANT: ZHANG, YING-XIN

APPLICANT: COX, TONY

APPLICANT: HUISMAN, GJALT

APPLICANT: YUAN, LING

APPLICANT: AFFHOLTER, JOSEPH A.

TITLE OF INVENTION: EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE

RECOMBINATION

FILE REFERENCE: 02-020730US

CURRENT APPLICATION NUMBER: US/09/354,922

CURRENT FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 358

TYPE: PRT

ORGANISM: Escherichia coli

SEQUENCE 358 AA; 38462 MW; 630763 CN;

Query Match 100.0%; Score 140; DB 18; Length 358;
Best Local Similarity 76.9%; Pred. No. 3.58e-06;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 46 ISTGSLDIALGAGGLPMGRIVEY 71
||| ||||| ||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 9
ID US-09-370-319-17 STANDARD; PRT; 363 AA.

XX AC xxxxxx

Sequence 17, Application US/09370319

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Morgante, Michele

CC APPLICANT: Sakai, Hajime
CC TITLE OF INVENTION: DNA Repair Proteins
CC FILE REFERENCE: BB-1204

CC CURRENT APPLICATION NUMBER: US/09/370,319

CC CURRENT FILING DATE: 1999-08-09

CC EARLIER APPLICATION NUMBER: 60/096,239

CC EARLIER FILING DATE: August 12, 1998

CC NUMBER OF SEQ ID NOS: 22

CC SOFTWARE: Microsoft Office 97

CC SEQ ID NO 17

CC LENGTH: 363

CC TYPE: PRT

CC ORGANISM: Agrobacterium tumefaciens

CC SEQUENCE 363 AA; 38802 MW; 629047 CN;

Query Match 90.0%; Score 126; DB 18; Length 363;

Best Local Similarity 65.4%; Pred. No. 1.31e-04;

Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 51 VSTGSLDIALGIGLPGRIEY 76

||| ||||| ||| |||||

QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 10

ID US-09-328-352-7563 STANDARD; PRT; 355 AA.

XX AC xxxxxx

XX AC xxxxxx

XX AC xxxxxx

XX AC xxxxxx

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Run on: Tue Apr 25 12:26:46 2000; Maspar time 4.03 Seconds
Tabular output not generated. 258.571 Million cell updates/sec

Title: >seqlmod
Description: (1-26) from 103.pgp
Perfect Score: 140
Sequence: 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

Scoring table: PAM 150
Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir62
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 30.173; Variance 52.165; scale 0.578

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	140	100.0	353	1 RQECA	recombination protein	3.48e-13
2	140	100.0	354	2 S31481	recombination protein	3.48e-13
3	140	100.0	356	2 S37586	recombination protein	3.48e-13
4	138	98.6	348	2 J01461	recombination protein	8.76e-13
5	130	92.9	354	2 A49299	recombination protein	3.40e-11
6	128	91.4	360	2 I40347	recombination protein	8.42e-11
7	127	90.7	346	1 RQPSAA	recombination protein	1.32e-10
8	127	90.7	348	1 A60989	recombination protein	1.32e-10
9	127	90.7	349	2 JN0321	recombination protein	1.32e-10
10	127	90.7	352	2 JC2406	recombination protein	1.32e-10
11	127	90.7	352	2 A47709	recombination protein	1.32e-10
12	126	90.0	349	2 I39509	recombination protein	1.32e-10
13	126	90.0	354	2 S46274	recombination protein	2.08e-10
14	126	90.0	355	1 RQEBPM	recombination protein	2.08e-10
15	126	90.0	363	2 J13777	recombination protein	2.08e-10
16	123	87.9	344	2 J00776	recombination protein	7.97e-10
17	123	87.9	348	2 S16898	recombination protein	7.97e-10
18	123	87.9	348	2 JN0639	recombination protein	7.97e-10
19	123	87.9	351	2 S16896	recombination protein	7.97e-10
20	121	86.4	342	2 S18728	recombination protein	1.94e-09
21	121	86.4	347	1 RQPSAC	recombination protein	1.94e-09
22	120	85.7	355	2 S49464	recombination protein	3.03e-09
23	119	85.0	353	2 JC5198	recombination protein	4.72e-09

24	118	84.3	343	2	S41560	recombination protein	7.35e-09
25	118	84.3	343	2	JC4718	recombination protein	7.35e-09
26	115	82.1	274	2	S24742	recombination protein	2.75e-08
27	115	82.1	274	2	S24745	recombination protein	2.75e-08
28	115	82.1	340	2	E64237	recombination protein	2.75e-08
29	115	82.1	711	2	S37025	recombination protein	2.75e-08
30	113	80.7	340	2	A55288	recombination protein	6.59e-08
31	113	80.7	347	2	S58683	recombination protein	6.59e-08
32	113	80.7	347	2	G71967	recombination protein	6.59e-08
33	113	80.7	387	2	JC4578	recombination protein	6.59e-08
34	112	80.0	340	2	JX0292	recombination protein	1.02e-07
35	112	80.0	340	2	C55020	recombination protein	1.02e-07
36	112	80.0	365	2	B48945	recombination protein	1.02e-07
37	111	79.3	346	1	RQBCAT	recombination protein	1.57e-07
38	111	79.3	790	2	S18206	recombination protein	1.57e-07
39	110	78.6	336	2	S73678	recombination protein	2.42e-07
40	107	76.4	388	2	S30219	recombination protein	8.79e-07
41	106	75.7	348	2	J00745	recombination protein	1.35e-06
42	106	75.7	352	2	H71488	recombination protein	1.35e-06
43	106	75.7	354	2	S76945	recombination protein	1.35e-06
44	104	74.3	354	2	S41764	recombination protein	3.15e-06
45	103	73.6	344	2	S08222	recombination protein	4.81e-06

ALIGNMENTS

RESULT 1

ENTRY

TITLE

ALTERNATE_NAMES

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#accession

##status

##molecule_type

##residues

##cross-references

##experimental_source

#authors

#journal

#title

#cross-references

#accession

##molecule_type

##residues

##cross-references

#authors

#journal

#title

#cross-references

#accession

##molecule_type

##residues

##cross-references

#authors

#journal

#title

#cross-references

#accession

##molecule_type

##residues

##cross-references

#authors

#journal

#title

```

Db      41 ISTGSLSDIALGAGGLPMGRIVEY 66
|||||
QY      1 ISTXSLSDIALXXXXLPMXRIVEY 26

RESULT 2
ENTRY   S31481          #type complete
TITLE   recombination protein recA - Enterobacter agglomerans
        recombinase A
ALTERNATE_NAMES
ORGANISM #formal_name Enterobacter agglomerans
DATE     13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
        05-Mar-1999
ACCESSIONS
REFERENCE S31481
#authors Rappold, C.S.J.; Klingmueller, W.
#submission submitted to the EMBL Data Library, January 1993
#description Cloning and sequencing of the recA gene from Enterobacter
            agglomerans 339.
            #accession S31481
            ##status preliminary
            ##molecule_type DNA
            ##residues 1-354 ##label RAP
            ##cross-references GB:L03291; EMBL:Z19517; NID:g1209306; PID:g1209308
GENETICS
#gene recA
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
         response
FEATURE
67-74    #region nucleotide-binding motif A (P-loop)\
141-146  #region nucleotide-binding motif B\
73       #binding_site ATP (lys) #status predicted
SUMMARY  #length 354 #molecular-weight 37898 #checksum 7629
Query Match 100.0%; Score 140; DB 2; Length 354;
Best Local Similarity 76.9%; Pred. No. 3,48e-13;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db      41 ISTGSLSDIALGAGGLPMGRIVEY 66
|||||
QY      1 ISTXSLSDIALXXXXLPMXRIVEY 26

RESULT 3
ENTRY   S37586          #type complete
TITLE   recombination protein recA - Yersinia pestis
        recombinase A
ALTERNATE_NAMES
ORGANISM #formal_name Yersinia pestis
DATE     06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
        05-Mar-1999
ACCESSIONS
REFERENCE S37586
#authors Kryukov, V.M.; Suchkov, I.Y.; Sazykin, I.S.; Mishankin, B.N.
#submission submitted to the EMBL Data Library, October 1993
#description Complete nucleotide sequence of Yersinia pestis recA gene.
#accession S37586
##status preliminary
##molecule_type DNA
##residues 1-356 ##label KRY
##cross-references EMBL:X75336; NID:g406793; PID:g406794
GENETICS
#gene recA
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
         response
FEATURE
67-74    #region nucleotide-binding motif A (P-loop)\
141-146  #region nucleotide-binding motif B\
73       #binding_site ATP (Lys) #status predicted
SUMMARY  #length 356 #molecular-weight 37912 #checksum 8556
Query Match 100.0%; Score 140; DB 2; Length 356;
Best Local Similarity 76.9%; Pred. No. 3,48e-13;

```

```

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLDLIALGAGGLPMGRIVEIY 66
   ||| ||||| ||| |||||
QY 1 ISTXSLDLIALXXXXLPMXRIVEIY 26

RESULT 4
ENTRY JQ1461 #type complete
TITLE recombination protein recA - Vibrio anguillarum
ALTERNATE_NAMES recombinationase A
ORGANISM formal_name Vibrio anguillarum
DATE 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
05-Mar-1999

ACCESSIONS JQ1461
REFERENCE JQ1461
#authors Tolmasy, M.E.; Gamble, A.E.; Crosa, J.H.
#journal Gene (1992) 110:41-48
#title Characterization of the recA gene of Vibrio anguillarum.
#cross-references MUID:92184113
#accession JQ1461
#molecule_type DNA
#residues 1-348 #label TOL
#cross-references GB:M80525; NID:g155256; PID:g155257
#experimental_source strains 775 and 531A

GENETICS
#gene recA
#description plays an essential role in homologous recombination, in
induction of the SOS response, and in initiation of stable
DNA replication
CLASSIFICATION #region nucleotide-binding motif A (P-loop)\
KEYWORDS #region nucleotide-binding motif B\
ATP: DNA binding; DNA recombination; DNA repair; P-loop; SOS
response

FEATURE 65-72 #region nucleotide-binding motif A (P-loop)\
139-144 #region nucleotide-binding motif B\
256-279 #region ATP binding #status predicted\
71 #binding_site ATP (Lys) #status predicted
SUMMARY #length 348 #molecular-weight 37558 #checksum 5094

Query Match 98.6%; Score 138; DB 2; Length 348;
Best Local Similarity 73.1%; Pred. No. 8.76e-13;
Matches 19; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLDLIALGAGGLPMGRIVEIY 64
   ||| ||||| ||| |||||
QY 1 ISTXSLDLIALXXXXLPMXRIVEIY 26

RESULT 5
ENTRY A49929 #type complete
TITLE recombination protein recA - Haemophilus influenzae (strain
Rd KW20)
ALTERNATE_NAMES rec-1 protein; recombinationase A
ORGANISM formal_name Haemophilus influenzae
DATE 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
17-Mar-1999

ACCESSIONS A49929; A64080
REFERENCE A49929
#authors Zulty, J.J.; Barcak, G.J.
#journal J. Bacteriol. (1993) 175:7269-7281
#title Structural organization, nucleotide sequence, and regulation
of the Haemophilus influenzae rec-1(+) gene.
#cross-references MUID:94042901
#accession A49929
#molecule_type DNA
#residues 1-354 #label ZUL
#cross-references GB:L07529; NID:g305381; PID:g305382
#experimental_source Rd strain KW20

REFERENCE A64000
#authors Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.;
Kirkness, E.F.; Kerlavage, A.R.; Bult, C.J.; Tomb, J.F.;

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Dougherty, B.A.; Merrick, J.M.; McKenney, K.; Sutton, G.;
Fitzhugh, W.; Fields, C.; Gocayne, J.D.; Scott, J.;
Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
J.F.; Phillips, C.A.; Spriggs, T.; Hedblom, E.; Cotton,
M.D.; Utterback, T.R.; Hanna, M.C.; Nguyen, D.T.; Sauddek,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann,
J.L.; Geoghagen, N.S.M.; Gnehm, C.L.; McDonald, L.A.;
Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.C.
Science (1995) 269:496-512
Whole-genome random sequencing and assembly of Haemophilus
influenzae Rd.
#cross-references MUID:95350630
#accession A64080
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-354 #label TIGR
#cross-references GB:U32741; GB:L42023; NID:g1573582; PID:g1573588;
TIGR:HI0600
#experimental_source Rd strain KW20

GENETICS
#gene recA
#description plays an essential role in homologous recombination, in
induction of the SOS response, and in initiation of stable
DNA replication
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS ATP: DNA binding; DNA recombination; DNA repair; P-loop; SOS
response

FEATURE 67-74 #region nucleotide-binding motif A (P-loop)\
141-146 #region nucleotide-binding motif B\
73 #binding_site ATP (Lys) #status predicted
SUMMARY #length 354 #molecular-weight 38132 #checksum 9408

Query Match 92.9%; Score 130; DB 2; Length 354;
Best Local Similarity 65.4%; Pred. No. 3.40e-11;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLDLIALGAGGLPMGRIVEIY 66
   ||| ||||| ||| |||||
QY 1 ISTXSLDLIALXXXXLPMXRIVEIY 26

RESULT 6
ENTRY I40347 #type complete
TITLE recombination protein recA - Brucella abortus
ALTERNATE_NAMES recombinationase A
ORGANISM formal_name Brucella abortus
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
05-Mar-1999

ACCESSIONS I40347
REFERENCE I40347
#authors Tatum, F.M.
#journal Microb. Pathog. (1993) 14:177-185
#title Construction of a Brucella abortus recA mutant and its
survival in mice.
#cross-references MUID:93309295
#accession I40347
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-360 #label RES
#cross-references GB:L00679; NID:g144122; PID:g144123

GENETICS
#gene recA
#description #superfamily recombination protein recA
CLASSIFICATION ATP: DNA binding; DNA recombination; DNA repair; P-loop; SOS
KEYWORDS response

FEATURE 77-84 #region nucleotide-binding motif A (P-loop)\
151-156 #region nucleotide-binding motif B\
83 #binding_site ATP (Lys) #status predicted
SUMMARY #length 360 #molecular-weight 38668 #checksum 4930

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```

Query Match          91.4%; Score 128; DB 2; Length 360;
Best Local Similarity 69.2%; Pred. No. 8.42e-11;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 51 VSTGSLDIALGVLGPKRIVEY 76
      :||| ||||| ||| :||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 7
ENTRY ROPSA #type complete
TITLE recombination protein reca - Pseudomonas aeruginosa
ALTERNATE_NAMES recombination A
ORGANISM #formal_name Pseudomonas aeruginosa
DATE 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change
05-Mar-1999
ACCESSIONS S06265; S10458; A49854; JN0304
REFERENCE S06265
#authors Sano, Y.; Kageyama, M.
#journal Mol. Gen. Genet. (1987) 208:412-419
#title The sequence and function of the reca gene and its protein in
# Pseudomonas aeruginosa PAO.
#cross-references MUID:88038334
#accession S06265
#molecule_type DNA
#residues 1-346 #label SANI
#cross-references GB:X05891; NID:g45413; PID:g45414
#note part of this sequence, including the amino end of the
mature protein, was confirmed by protein sequencing

REFERENCE S10458
#authors Zaitsev, E.N.; Krjukov, V.M.; Kuzmin, N.P.; Alekseev, A.A.;
Lanzov, V.A.
#submission submitted to the EMBL Data Library, March 1990
#description Restriction polymorphism and nucleotide sequence
substitutions in the reca gene of Pseudomonas aeruginosa
strains.
#accession S10458
#molecule_type DNA
#residues 1-346 #label ZAI
#cross-references EMBL:X52261; NID:g45383; PID:g45384
REFERENCE A49854
#authors Sano, Y.
#journal J. Bacteriol. (1993) 175:2451-2454
#title Role of the reca-related gene adjacent to the reca gene in
Pseudomonas aeruginosa.
#cross-references MUID:93224470
#accession A49854
#status preliminary
#molecule_type DNA
#residues 313-346 #label SAN2
#cross-references GB:D13090; NID:g286185
#note sequence extracted from NCBI backbone (NCBIN:129317,
NCBIN:129318)

REFERENCE JN0304
#authors Krjukov, V.M.; Zaitsev, E.N.; Kouzmin, N.P.; Bayev, A.A.
#journal Bioorg. Khim. (1990) 16:1177-1182
#title Structure of the reca gene from Pseudomonas aeruginosa.
#cross-references MUID:91182156
#accession JN0304
#molecule_type DNA
#residues 1-332, 1', 334-346 #label KRY
#cross-references GB:X52261; NID:g45383; PID:g45384
#experimental_source strain PAO 7
#note the authors translated the codon CTG for residue 333 as
val

GENETICS
#gene reca
FUNCTION
#description plays an essential role in homologous recombination, in
induction of the SOS response, and in initiation of stable
DNA replication
#superfamily recombination protein reca
CLASSIFICATION
#superfamily recombination protein reca
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS

```

```

response
FEATURE 65-72 #region nucleotide-binding motif A (P-loop)\
139-144 #region nucleotide-binding motif B\
71 #binding_site ATP (Lys) #status predicted
SUMMARY #length 346 #molecular-weight 36879 #checksum 5795

Query Match          90.7%; Score 127; DB 1; Length 346;
Best Local Similarity 69.2%; Pred. No. 1.32e-10;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLDIALGIGLPGKRIEY 64
      :||| ||||| ||| :||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 8
ENTRY A60989 #type complete
TITLE recombination protein reca - Legionella pneumophila
ALTERNATE_NAMES recombinationase A
ORGANISM #formal_name Legionella pneumophila
DATE 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change
05-Mar-1999
ACCESSIONS A60989
REFERENCE A60989
#authors Zhao, X.; Dreyfus, L.A.
#journal FEMS Microbiol. Lett. (1990) 70:227-232
#title Expression and nucleotide sequence analysis of the Legionella
pneumophila reca gene.
#accession A60989
#molecule_type DNA
#residues 1-348 #label ZHA
#cross-references GB:X55453; NID:g48779; PID:g48780
GENETICS
#gene reca
FUNCTION
#description plays an essential role in homologous recombination, in
induction of the SOS response, and in initiation of stable
DNA replication
CLASSIFICATION
#superfamily recombination protein reca
KEYWORDS ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
response

FEATURE 66-73 #region nucleotide-binding motif A (P-loop)\
140-145 #region nucleotide-binding motif B\
72 #binding_site ATP (Lys) #status predicted
SUMMARY #length 348 #molecular-weight 37934 #checksum 1920

Query Match          90.7%; Score 127; DB 1; Length 348;
Best Local Similarity 69.2%; Pred. No. 1.32e-10;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLDIALGIGLPGKRIEY 65
      :||| ||||| ||| :||| |||||
QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 9
ENTRY JN0321 #type complete
TITLE recombination protein reca - Azotobacter vinelandii
ALTERNATE_NAMES recombinationase A
ORGANISM #formal_name Azotobacter vinelandii
DATE 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change
05-Mar-1999
ACCESSIONS JN0321
REFERENCE JN0321
#authors Kenkatesh, T.V.; Das, H.K.
#journal Gene (1992) 113:47-53
#title The Azotobacter vinelandii reca gene: sequence analysis and
regulation of expression.
#cross-references MUID:92225347
#accession JN0321
#molecule_type DNA

```



```

#title      Characterization of the recA gene from Pseudomonas
#            fluorescens OE 28.3 and construction of a recA mutant.
#cross-references MUID:93195512
#contents   OE 28.3
#accession  A47709
#status     preliminary
#molecule_type nucleic acid
#residues   1-352 ##label DE1
#cross-references GB:M96558; NID:g151529; PID:g151530
#note       sequence extracted from NCBI backbone (NCBIN:127247,
            NCBIP:127246)

CLASSIFICATION
KEYWORDS    #superfamily recombination protein recA
            ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
            response

FEATURE
55-72       #region nucleotide-binding motif A (P-loop)\
139-144     #region nucleotide-binding motif B\
71          #binding_site ATP (lys) #status predicted
SUMMARY     #length 352 #molecular-weight 37634 #checksum 9671

Query Match          90.7%; Score 127; DB 2; Length 352;
Best Local Similarity 69.2%; Pred. No. 1.32e-10;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLGLDIALGIGLPKGRIVEY 64
QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26

RESULT 12
ENTRY   #type complete
TITLE   recombination protein recA - Acinetobacter calcoaceticus
ALTERNATE_NAMES
ORGANISM Acinetobacter calcoaceticus
DATE     19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
        05-Mar-1999
ACCESSION I39509
REFERENCE I39509
#authors  Gregg-Jolly, L.A.; Ornstom, L.N.
#journal  Mol. Microbiol. (1994) 12:985-992
#title    Properties of Acinetobacter calcoaceticus recA and its
            contribution to intracellular gene conversion.
#cross-references MUID:95020620
#accession I39509
#status    preliminary; translated from GB/EMBL/DDBJ
#molecule_type DNA
#residues  1-349 ##label RES
#cross-references GB:L26100; NID:g440088; PID:g440089
GENETICS
#gene      recA
CLASSIFICATION
KEYWORDS   #superfamily recombination protein recA
            ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
            response

FEATURE
55-72       #region nucleotide-binding motif A (P-loop)\
139-144     #region nucleotide-binding motif B\
71          #binding_site ATP (lys) #status predicted
SUMMARY     #length 349 #molecular-weight 37815 #checksum 368

Query Match          90.0%; Score 126; DB 2; Length 349;
Best Local Similarity 65.4%; Pred. No. 2.08e-10;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 39 VSTGSLTLDIALGIGLPKGRIVEY 64
QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26

RESULT 13
ENTRY   #type complete
TITLE   recombination protein recA - Vibrio cholerae
ALTERNATE_NAMES
ORGANISM Acinetobacter calcoaceticus

```

```

DATE          27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
17-Mar-1999
ACCESSIONS    S46274
REFERENCE     S46274
#authors      Stroemer, U.H.; Lech, A.J.; Manning, P.A.
#journal      Mol. Gen. Genet. (1994) 244:295-302
#title        Gene sequence of recA(+) and construction of recA mutants of
              Vibrio cholerae.
#cross-references MUID:94335880
#accession    S46274
#status       preliminary
#molecule_type DNA
#residues     1-354 #label STR
#cross-references EMBL:X71969; NID:9530269; PID:9530270
GENETICS
#gene         recA
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS      ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
              response
FEATURE
65-72         #region nucleotide-binding motif A (P-loop)\
139-144       #region nucleotide-binding motif B\
71            #binding_site ATP (Lys) #status Predicted
#length 354 #molecular-weight 38273 #checksum 1962
SUMMARY
Query Match   90.0%; Score 126; DB 2; Length 354;
Best Local Similarity 72.0%; Pred. No. 2.08e-10;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Db 39 ISTGSLDITLGGGLPMGRIVEI 63
QY 1 ISTXSLSLDIALXXXLPMXRIVEI 25

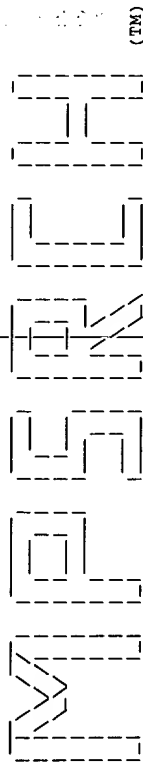
RESULT 14
ENTRY      RQBPM #type complete
TITLE      recombination protein recA - Proteus mirabilis
ALTERNATE_NAMES
ORGANISM    #formal_name Proteus mirabilis
DATE        30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change
05-Mar-1999
ACCESSIONS S04606
REFERENCE   S04606
#authors    Akaboshi, E.; Yip, M.L.R.; Howard-Flanders, P.
#journal     Nucleic Acids Res. (1989) 17:4390
#title       Nucleotide sequence of the recA gene of Proteus mirabilis.
#cross-references MUID:89296502
#accession   S04606
#molecule_type DNA
#residues    1-355 #label AKA
#cross-references GB:X14870; NID:945631; PID:945632
ETICS
#gene       recA
FUNCTION     plays an essential role in homologous recombination, in
              induction of the SOS response, and in initiation of stable
              DNA replication
CLASSIFICATION #superfamily recombination protein recA
KEYWORDS      ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
              response
FEATURE
67-74       #region nucleotide-binding motif A (P-loop)\
141-146     #region nucleotide-binding motif B\
73          #binding_site ATP (Lys) #status Predicted
#length 355 #molecular-weight 38219 #checksum 901
SUMMARY
Query Match   90.0%; Score 126; DB 1; Length 355;
Best Local Similarity 69.2%; Pred. No. 2.08e-10;
Matches 18; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Db 41 ISTGSLDVALGGLPMGRIVEIY 66
QY 1 ISTXSLSLDIALXXXLPMXRIVEIY 26

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RESULT 15
ENTRY      JCI377 #type complete
TITLE      recombination protein recA - Agrobacterium tumefaciens
ALTERNATE_NAMES
ORGANISM    #formal_name Agrobacterium tumefaciens
DATE        10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change
17-Mar-1999
ACCESSIONS JCI377
REFERENCE   JCI377
#authors    Wardhan, H.; McPherson, M.J.; Harris, C.A.; Sharma, E.;
              Sastry, G.R.K.
#journal     Gene (1992) 121:133-136
#title       Molecular analysis of the recA gene of Agrobacterium
              tumefaciens C58.
#cross-references MUID:93051348
#accession   JCI377
#molecule_type DNA
#residues    1-363 #label WAR
#cross-references GB:M36776
GENETICS
#gene       recA
FUNCTION     plays an essential role in homologous recombination, in
              induction of the SOS response, and in initiation of stable
              DNA replication
              #superfamily recombination protein recA
              ATP; DNA binding; DNA recombination; DNA repair; P-loop; SOS
              response
CLASSIFICATION
KEYWORDS
FEATURE
77-84       #region nucleotide-binding motif A (P-loop)\
151-156     #region nucleotide-binding motif B\
83          #binding_site ATP (Lys) #status Predicted
#length 363 #molecular-weight 38802 #checksum 7164
SUMMARY
Query Match   90.0%; Score 126; DB 2; Length 363;
Best Local Similarity 65.4%; Pred. No. 2.08e-10;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 51 VSTGSLSLDIALGGLPKGRIVEIY 76
QY 1 ISTXSLSLDIALXXXLPMXRIVEIY 26
Search completed: Tue Apr 25 12:26:54 2000
Job time : 8 secs.

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 (TM)

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MPPerch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Apr 25 12:27:11 2000; MasPar time 18.89 seconds
 Tabular output not generated. 41,102 Million cell updates/sec

Title: >seq1mod
 Description: (1-26) from 103.pep
 Perfect Score: 140
 Sequence: 1 ISTXSLSLDIALXXXXLPMXGRIVEIY 26

Scoring table: PAM 150
 Gap 15

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 31.021; Variance 45.862; scale 0.676

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	140	100.0	325	1	RECA_PROVU RECA PROTEIN.	1.05e-15
2	140	100.0	352	1	RECA_ECOLI RECA PROTEIN.	1.05e-15
3	140	100.0	352	1	RECA_SHISO RECA PROTEIN.	1.05e-15
4	140	100.0	354	1	RECA_ENTAG RECA PROTEIN.	1.05e-15
5	140	100.0	354	1	RECA_SERMA RECA PROTEIN.	1.05e-15
6	140	100.0	356	1	RECA_YERPE RECA PROTEIN.	1.05e-15
7	140	100.0	358	1	RECA_XENBV RECA PROTEIN.	1.05e-15
8	138	98.6	348	1	RECA_VIBAN RECA PROTEIN.	3.08e-15
9	135	96.4	354	1	RECA_VIBCH RECA PROTEIN.	1.50e-14
10	131	93.6	354	1	RECA_PASMU RECA PROTEIN.	1.24e-13
11	130	92.9	354	1	RECA_BRAIN RECA PROTEIN. (RECOMBIN	2.10e-13
12	128	91.4	360	1	RECA_BRUAB RECA PROTEIN.	5.99e-13
13	127	90.7	346	1	RECA_PSEAE RECA PROTEIN.	1.01e-12
14	127	90.7	348	1	RECA_LSPGN RECA PROTEIN.	1.01e-12
15	127	90.7	349	1	RECA_AGOVI RECA PROTEIN.	1.01e-12
16	127	90.7	352	1	RECA_PSEFL RECA PROTEIN.	1.01e-12
17	127	90.7	355	1	RECA_PSEPU RECA PROTEIN.	1.01e-12
18	126	90.0	342	1	RECA_ERWCA RECA PROTEIN.	1.70e-12
19	126	90.0	349	1	RECA_ACICA RECA PROTEIN.	1.70e-12
20	126	90.0	354	1	RECA_PROMI RECA PROTEIN.	1.70e-12
21	126	90.0	363	1	RECA_AGRTU RECA PROTEIN.	1.70e-12
22	125	89.3	361	1	RECA_RHLP RECA PROTEIN.	2.86e-12
23	123	87.9	344	1	RECA_METFL RECA PROTEIN.	8.05e-12

24	123	87.9	348	1	RECA_ACEPO RECA PROTEIN.	8.05e-12
25	123	87.9	351	1	RECA_RHIME RECA PROTEIN.	8.05e-12
26	123	87.9	351	1	RECA_RHILY RECA PROTEIN.	8.05e-12
27	121	86.4	342	1	RECA_METCL RECA PROTEIN.	2.25e-11
28	121	86.4	344	1	RECA_GLUOX RECA PROTEIN.	2.25e-11
29	121	86.4	347	1	RECA_BURCE RECA PROTEIN.	2.25e-11
30	120	85.7	355	1	RECA_RHOCA RECA PROTEIN.	3.77e-11
31	119	85.0	353	1	RECA_AERSA RECA PROTEIN.	6.28e-11
32	118	84.3	343	1	RECA_XANCP RECA PROTEIN.	1.05e-10
33	118	84.3	343	1	RECA_RHOSH RECA PROTEIN.	1.05e-10
34	118	84.3	344	1	RECA_XANCI RECA PROTEIN.	1.05e-10
35	118	84.3	344	1	RECA_XANOR RECA PROTEIN.	1.05e-10
36	118	84.3	348	1	RECA_RHOVI RECA PROTEIN.	1.05e-10
37	115	82.1	274	1	RECA_NEIMI RECA PROTEIN (FRAGMENT	1.05e-10
38	115	82.1	274	1	RECA_NEIME RECA PROTEIN (FRAGMENT	4.80e-10
39	115	82.1	340	1	RECA_MYCGE RECA PROTEIN.	4.80e-10
40	115	82.1	348	1	RECA_NEIGO RECA PROTEIN.	4.80e-10
41	115	82.1	711	1	RECA_MYCLE RECA PROTEIN.	4.80e-10
42	113	80.7	340	1	RECA_RICPR RECA PROTEIN.	1.32e-09
43	113	80.7	356	1	RECA_PARDE RECA PROTEIN.	1.32e-09
44	113	80.7	377	1	RECA_STRVL RECA PROTEIN.	1.32e-09
45	113	80.7	387	1	RECA_LEPBI RECA PROTEIN.	1.32e-09

ALIGNMENTS

RESULT 1
 ID RECA_PROVU STANDARD; PRT: 325 AA.
 AC P26346;

DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.

GN RECA.

OS Proteus vulgaris.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.

RN [1]

RP SEQUENCE FROM N.A.

RA ZHAO X., MCENTEE K.;

RA MEDLINE; 91109725.

RT "DNA sequence analysis of the recA genes from Proteus vulgaris,
 RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
 RL Mol. Gen. Genet. 222:369-376(1990).

CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.

CC SIMILARITY: BELONGS TO THE RECA FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; X55355; ; NOT_ANNOTATED_CDS.

DR HSP; P03017; 2REB.

DR PROSITE; PS00321; RECA; 1.

DR PFW; PF00154; reca; 1.

KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 NP_BIND 67 74 ATP (BY SIMILARITY).

SQ SEQUENCE 325 AA; 34790 MW; D46C9851 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 325;
 Best Local Similarity 76.9%; Pred. No. 1.05e-15;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 41 ISTXSLSLDIALGAGGLPMXGRIVEIY 66


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FT HELIX 146 148
FT TURN 152 155
FT HELIX 166 185
FT TURN 186 186
FT STRAND 188 193
FT HELIX 213 218
FT STRAND 221 233
FT TURN 234 235
FT STRAND 236 249
FT STRAND 257 263
FT TURN 264 266
FT STRAND 267 268
FT HELIX 270 280
FT TURN 281 282
FT STRAND 285 287
FT TURN 288 289
FT STRAND 290 293
FT TURN 294 295
FT STRAND 296 300
FT HELIX 301 311
FT HELIX 313 327
SQ SEQUENCE 352 AA; 37842 MW; A6DE5451 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 352;
Best Local Similarity 76.9%; Pred. No. 1.05e-15;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLSLDIALGAGLPMGRIVEYI 65
QY 1 ISTXSLSLDIALXXXXLPMXRIEYI 26

RESULT 3
ID RECA_SHISO STANDARD; PRT; 352 AA.
AC Q92FF6;
DT 15-DEC-1999 (Rel. 39, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Shigella sonnei.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-KNH104S;
CC PARK Y.C., SHIN H.J., KIM Y.C.;
CC "Cloning and nucleotide sequence of the recA gene from Shigella sonnei KNH104S."
CC Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
CC !- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC EMBL; AF101227; AAC72856.1;
CC PROSITE; PS00321; RECA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 66 73
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
CC SEQUENCE 352 AA; 37799 MW; ADE29D96 CRC32;

FT INIT_MET 0 0 BY SIMILARITY.
FT NP_BIND 66 73 ATP (POTENTIAL).
SQ SEQUENCE 352 AA; 37799 MW; ADE29D96 CRC32;

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Query Match 100.0%; Score 140; DB 1; Length 352;
Best Local Similarity 76.9%; Pred. No. 1.05e-15;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLSLDIALGAGLPMGRIVEYI 65
QY 1 ISTXSLSLDIALXXXXLPMXRIEYI 26

RESULT 4
ID RECA_ENTAG STANDARD; PRT; 354 AA.
AC P33037;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Enterobacter agglomerans.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pantoea.
CC [1]
CC SEQUENCE FROM N.A.
CC RAPPOLD C.S.J., KLINGMUELLER W.;
CC Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
CC !- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC EMBL; L03291; AAA91766.1;
CC PIR; S31481; S31481.
CC HSSP; P03017; 2REB.
CC PROSITE; PS00321; RECA; 1.
CC PFAM; PF00154; RECA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
CC SEQUENCE 354 AA; 37898 MW; 629E3B60 CRC32;

Query Match 100.0%; Score 140; DB 1; Length 354;
Best Local Similarity 76.9%; Pred. No. 1.05e-15;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSLDIALGAGLPMGRIVEYI 66
QY 1 ISTXSLSLDIALXXXXLPMXRIEYI 26

RESULT 5
ID RECA_SERMA STANDARD; PRT; 354 AA.
AC P17479;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-SM6;
CC MEDLINE; 90094239.

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RA BALL T.K., WASMUTH C.R., BRAUNAGEL S.C., BENEDIK M.J.;
RT "Expression of Serratia marcescens extracellular proteins requires
RE reca".
RL J. Bacteriol. 172:342-349(1990).
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
CC EMBL: M22935; AAA26567.1; -.
CC DR HSSP: P03017; 2REB.
CC DR PROSITE: PS00321; RECA; 1.
CC PFAM: PF00154; reca; 1.
CC KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC FT NP_BIND 67 74 ATP (BY SIMILARITY)
CC SQ SEQUENCE 354 AA; 37909 MW; 2BC62FDE CRC32;

Query Match 100.0%; Score 140; DB 1; Length 354;
Best Local Similarity 76.9%; Pred. No. 1.05e-15;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSLDIALGAGGLPMGRIVEY 66
QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26

RESULT 6
ID RECA.YERPE STANDARD; PRT; 356 AA.
AC P37858;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
CC Versinia pestis.
CC OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Yersinia.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=231;
CC KRYUKOV V.M., SUCHKOV I.Y., SAZYKIN I.S., MISHANKIN B.N.;
CC Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X75336; CAA53084.1; -.
CC DR PIR: S37586; S37586.
CC DR HSSP: P03017; 2REB.
CC DR PROSITE: PS00321; RECA; 1.

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DR PFAM: PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (BY SIMILARITY)
SQ SEQUENCE 356 AA; 37912 MW; 60B356BF CRC32;

Query Match 100.0%; Score 140; DB 1; Length 356;
Best Local Similarity 76.9%; Pred. No. 1.05e-15;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSLDIALGAGGLPMGRIVEY 66
QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26

RESULT 7
ID RECA.XENBV STANDARD; PRT; 358 AA.
AC P96185;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
CC Xenorhabdus bovienii.
CC OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Xenorhabdus.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=T28/1;
CC RALSTON R.A., GRMSBY R., RALSTON H., THOMAS C.J.;
CC Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
CC EMBL: U87924; AAD12585.1; -.
CC DR HSSP: P03017; 2REB.
CC DR PROSITE: PS00321; RECA; 1.
CC KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC FT NP_BIND 67 74 ATP (POTENTIAL)
CC SQ SEQUENCE 358 AA; 38487 MW; 35B7853C CRC32;

Query Match 100.0%; Score 140; DB 1; Length 358;
Best Local Similarity 76.9%; Pred. No. 1.05e-15;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLSLDIALGAGGLPMGRIVEY 66
QY 1 ISTXSLSLDIALXXXLPMXRIVEY 26

RESULT 8
ID RECA.VIBAN STANDARD; PRT; 348 AA.
AC P26348;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
CC Vibrio anguillarum.
CC OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

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RN RP SEQUENCE FROM N.A.
RX MEDLINE; 92236419.
RA GAMMIE A.E., CROSA J.H.;
RT "Co-operative autoregulation of a replication protein gene.";
RL Mol. Microbiol. 5:3015-3023(1991).
RN RP SEQUENCE FROM N.A.
RX STRAIN-775 AND 531A;
RA MEDLINE; 92184113.
RA TOLMANSKY M.E., GAMMIE A.E., CROSA J.H.;
RT "Characterization of the recA gene of Vibrio anguillarum.";
RL Gene 110:41-48(1992).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
      PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
      SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
      HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
      WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
      CLEAVAGE.
CC
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC
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CC
CC EMBL; M80525; AAA27554.1; -
CC PIR; JQ1461; JQ1461.
CC DR HSSP; P03017; 2REB.
CC DR PROSITE; PS00321; RECA; 1.
CC DR PFAM; PF00154; RECA; 1.
CC DR DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 65 72 ATP (BY SIMILARITY).
CC FT CONFLICT 94 94 A -> T (IN REF. 2).
CC SQ SEQUENCE 348 AA; 37558 MW; FD418A1D CRC32;

Query Match 98.6%; Score 138; DB 1; Length 348;
Best Local Similarity 73.1%; Pred. No. 3 05e-15;
Matches 19; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLSLDIALGAGGLPMGRIVEY 64
   ||| ||||| ||| |||||
   1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 9
ID RECA_VIBCH STANDARD; PRT; 354 AA.
AC P45383;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-2740-80;
RA MEDLINE; 95129908.
RA MARGRAF R.L., ROCA A.I., COX M.M.;
RT "The deduced Vibrio cholerae RecA amino-acid sequence.";
RL Gene 152:135-136(1995).
RN RP SEQUENCE FROM N.A.
RC STRAIN-O17;
RX STROEHER U.H., LECH A.J., MANNING P.A.;
RT "Gene sequence of recA+ and construction of recA mutants of Vibrio
RT cholerae.";
RL Mol. Gen. Genet. 244:295-301(1994).
RN [3]

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RP REVISIONS TO 27: 49; 52 AND 64.
RX MEDLINE; 95129908.
RA MANNING P.A.;
RT Unpublished results, cited by:
RL MARGRAF R.L., ROCA A.I., COX M.M.;
RL Gene 152:135-136(1995).
RN RP SEQUENCE FROM N.A.
RC STRAIN-569B;
RA BHASIN N., GUPTA N., GHOSH A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
      PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
      SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
      HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
      WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
      CLEAVAGE.
CC
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC
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CC
CC EMBL; U10162; AAC43291.1; -
CC EMBL; X71969; CAA50764.1; ALT_SEQ.
CC DR EMBL; L42384; AAB59100.1; -
CC DR HSSP; P03017; 2REB.
CC DR PROSITE; PS00321; RECA; 1.
CC DR PFAM; PF00154; RECA; 1.
CC DR DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 65 72 ATP (POTENTIAL).
CC FT CONFLICT 94 94 A -> T (IN REF. 2).
CC SQ SEQUENCE 354 AA; 38250 MW; DF2E49E9 CRC32;

Query Match 96.4%; Score 135; DB 1; Length 354;
Best Local Similarity 73.1%; Pred. No. 1.50e-14;
Matches 19; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLSLDIALGAGGLPMGRIVEIF 64
   ||| ||||| ||| |||||
   1 ISTXSLSLDIALXXXXLPMXRIVEY 26

QY 1 ISTXSLSLDIALXXXXLPMXRIVEY 26

RESULT 10
ID RECA_PASMU STANDARD; PRT; 354 AA.
AC P95526;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-2.5;
RA BARBE GARCIA J.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
      PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
      SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
      HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
      WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
      CLEAVAGE.
CC
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
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DR EMBL: X99324; CAA67699.1; -
 DR HSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 DR PFW: PF00154; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 SQ SEQUENCE 354 AA; 37906 MW; 27DEED66 CRC32;

Query Match 93.6%; Score 131; DB 1; Length 354;
 Best Local Similarity 65.4%; Pred. No. 1.24e-13;
 Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 41 VSTGSLDVALGIGLPMGRIVEIF 66
 QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 11

ID RECA_HAEIN STANDARD; PRT; 354 AA.
 AC P43705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN (RECOMBINASE).
 GN RECA OR RECI OR HI0600.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD;
 RX MEDLINE: 95350630.
 RA ZULY J.J., BARCAK G.J.;
 RT "Structural organization, nucleotide sequence, and regulation of the
 RT Haemophilus influenzae rec-1+ gene."
 RL J. Bacteriol. 175:7269-7281(1993).

[2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20;
 RX MEDLINE: 95350630.
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
 RA KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
 RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
 RA SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
 RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
 RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,
 RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
 RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
 RA VENTER J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus
 RT influenzae Rd."
 RL Science 269:496-512(1995).

CC -1- FUNCTION: PLAYS A CENTRAL ROLE IN DNA METABOLISM, PARTICIPATING IN
 CC GENERAL HOMOLOGOUS RECOMBINATION, RECOMBINATIONAL
 CC (POSTREPLICATION) DNA REPAIR, AND PROPHAGE INDUCTION.

CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.
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DR EMBL: L07529; AAC36817.1; -
 DR EMBL: U32741; AAC22257.1; -

DR HSP: P03017; 2REB.
 DR TIGR: HI0600; -
 DR PROSITE: PS00321; RECA; 1.
 DR PFW: PF00154; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 SQ SEQUENCE 354 AA; 38132 MW; 52D4E68E CRC32;

Query Match 92.9%; Score 130; DB 1; Length 354;
 Best Local Similarity 65.4%; Pred. No. 2.10e-13;
 Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLDVALGIGLPMGRIVEIF 66
 QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 12

ID RECA_BRUAB STANDARD; PRT; 360 AA.
 AC Q04761;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Brucella abortus.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93309295.
 RA TATUM F.M.;
 RT "Construction of a Brucella abortus RecA mutant and its survival in
 RT mice."
 RL Microb. Pathog. 14:177-185(1993).
 CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -1- SIMILARITY: BELONGS TO THE RECA FAMILY.

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DR EMBL: L00679; AAA22999.1; -
 DR HSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 DR PFW: PF00154; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 77 84 ATP (BY SIMILARITY).
 SQ SEQUENCE 360 AA; 38668 MW; 6DBDF223 CRC32;

Query Match 91.4%; Score 128; DB 1; Length 360;
 Best Local Similarity 69.2%; Pred. No. 5.99e-13;
 Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 51 VSTGSLDIALGIGLPMGRIVEIF 76
 QY 1 ISTXSLDIALXXXXLPMXRIEY 26

RESULT 13

ID RECA_PSEAE STANDARD; PRT; 346 AA.
 AC P08280;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)


```

DE 15-DEC-1999 (Rel. 39, Last annotation update)
DN RECA.
GN Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-PAO.
RX MEDLINE; 88038334.
RA SANO Y., KAGEYAMA M.;
RT "The sequence and function of the recA gene and its protein in
RT Pseudomonas aeruginosa PAO.";
RT Mol. Gen. Genet. 208:412-419(1987).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-PAM 7;
RL ZAITSEV E.N., KRUKOV V.M., KUZMIN N.P., ALEKSEEV A.A., LANZOV V.A.;
RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE; 91182156.
RA KRIUKOV V.M., ZAITSEV E.N., KOUZMIN N.P., BAYEV A.A.;
RT "Structure of the Pseudomonas aeruginosa recA gene.";
RT Bioorg. Khim. 16:1177-1182(1990).
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
DR EMBL; X05691; CAA39173.1; -
DR EMBL; X52261; CAA36504.1; -
DR PIR; S06265; ROPSA.
DR PIR; S10458; S10458.
DR PIR; JN0304; JN0304.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; recA; 1.
DR NP_BIND 65 72 ATP (BY SIMILARITY).
FT CONFLICT 333 333 V -> L (IN REF. 3).
SQ SEQUENCE 346 AA; 36879 MW; 314B7320 CRC32;

Query Match 90.7%; Score 127; DB 1; Length 346;
Best Local Similarity 69.2%; Pred. No. 1.01e-12;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLGLDIALGIGGPKGRIVEY 64
QY 1 ISTXSLDLIALXXXLPMAIVEY 26

RESULT 14
ID RECA.LEGN STANDARD; PRT; 348 AA.
AC Q05358;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae;

15-DEC-1999 (Rel. 39, Last annotation update)
DN RECA.
GN Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-PAO.
RX MEDLINE; 88038334.
RA SANO Y., KAGEYAMA M.;
RT "The sequence and function of the recA gene and its protein in
RT Pseudomonas aeruginosa PAO.";
RT Mol. Gen. Genet. 208:412-419(1987).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-PAM 7;
RL ZAITSEV E.N., KRUKOV V.M., KUZMIN N.P., ALEKSEEV A.A., LANZOV V.A.;
RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE; 91182156.
RA KRIUKOV V.M., ZAITSEV E.N., KOUZMIN N.P., BAYEV A.A.;
RT "Structure of the Pseudomonas aeruginosa recA gene.";
RT Bioorg. Khim. 16:1177-1182(1990).
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X05691; CAA39173.1; -
DR EMBL; X52261; CAA36504.1; -
DR PIR; S06265; ROPSA.
DR PIR; S10458; S10458.
DR PIR; JN0304; JN0304.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; recA; 1.
DR NP_BIND 65 72 ATP (BY SIMILARITY).
FT CONFLICT 333 333 V -> L (IN REF. 3).
SQ SEQUENCE 346 AA; 36879 MW; 314B7320 CRC32;

Query Match 90.7%; Score 127; DB 1; Length 346;
Best Local Similarity 69.2%; Pred. No. 1.01e-12;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 39 ISTGSLGLDIALGIGGPKGRIVEY 64
QY 1 ISTXSLDLIALXXXLPMAIVEY 26

RESULT 14
ID RECA.LEGN STANDARD; PRT; 348 AA.
AC Q05358;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae;

```

```

OC Legionella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91032890.
RA ZHAO X., DREYFUS L.A.;
RT "Expression and nucleotide sequence analysis of the Legionella
RT FEMS Microbiol. Lett. 58:227-231(1990).
RL -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55453; CAA39097.1; -
DR EMBL; X55453; CAA39098.1; ALT_INIT.
DR PIR; A60989; A60989.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; recA; 1.
DR NP_BIND 66 73 ATP (BY SIMILARITY).
SQ SEQUENCE 348 AA; 37934 MW; 3BE33214 CRC32;

Query Match 90.7%; Score 127; DB 1; Length 348;
Best Local Similarity 69.2%; Pred. No. 1.01e-12;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 40 ISTGSLGLDIALGIGGPKGRIVEY 65
QY 1 ISTXSLDLIALXXXLPMAIVEY 26

RESULT 15
ID RECA.AZOVI STANDARD; PRT; 349 AA.
AC P29246;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Azotobacteraceae;
OC Azotobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9225347.
RA VENKATESH T.V., DAS H.K.;
RT "The Azotobacter vinelandii recA gene: sequence analysis and
RT regulation of expression.";
RL Gene 113:47-53(1992).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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! FINDPATTERNS on geneseq: * allowing 0 mismatches

! 1 IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)

1 W64215 ck: 6091 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS

W64216 ck: 5676 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS

W64217 ck: 6188 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS

W64218 ck: 6188 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS

W64213 ck: 6469 len: 358 ! New minshall recA protein. Evolution of wh
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS

W64214 ck: 7100 len: 358 ! Hyperrecombinogenic variant recA protein cl
IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
ISTGSLSDIALGAGGLPMGRIVEIY GPESS

Databases searched:

GeneSeq, Release 36.3, Released on 8Jul1999, Formatted on 9Jul1999

Total finds: 6
Total length: 23,686,106
Total sequences: 188,963
CPU time: 02:20.08

!!AA_SEQUENCE 1.0

ID W64215 standard; Protein; 358 AA.

AC W64215;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant recA protein clone 4.

KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN W09831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

DR Tobin MB;

DR WPI; 98-427565/36.

DR N-PSDB; V44287.

PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g.
CC enhanced recombinogenicity, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC recA protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

W64215 Length: 358 April 26, 2000 08:15 Type: P Check: 6091

1 MTGVNMAIDE NKOKALAAAL GOIEKQFGKG SIMRLGEDRC MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIRAAQ REGKTCAFID

101 AEHALDPIYA RLGVVDIDNL LCSQPDGEGQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEIEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSSETR

251 KVVKNKTAAP FKQAEFQILY GEGINFYGEL VDLGVKEKLI EKAGAWYSYK

301 GEKVGOQKAN ATAWLKDNP TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDE

!!AA_SEQUENCE 1.0

ID W64216 standard; Protein; 358 AA.

AC W64216;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant recA protein clone 5.

KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN W09831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

DR Tobin MB;

DR WPI; 98-427565/36.

DR N-PSDB; V44288.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of

CC recombination and selection/screening for evolution of whole cells

CC and organisms toward acquisition of desired properties, e.g.

CC enhanced recombinogenicity, genome copy number, and capacity for

CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC recA protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64216 Length: 358 April 26, 2000 08:15 Type: P Check: 5676

1 MTGVNMAIDE NKOKALAAAL GOIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLOVIRAAQ REGKTCAFID

101 AEHALDPIYA RLGVVDIDNL LCSQPDGEGQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEIEIGDSHM GLAARMMSQA MRKLGNLKL SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSSETR

251 KVVKNKIAAP FKQAEFQILY DEGINFYGEL VDLGVKELI EKAGAWYSYK
 301 GEKAGOGKAN AAWLKGNP TAKEIEKKVR ELLSNPNST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64217 standard; Protein: 358 AA.
 AC W64217;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 6.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-Al.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 Tobin MB;
 WPI: 98-427565/36.
 N-PSDB; V44289.
 DR Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see W64213), from an example of the present invention.
 SQ Sequence 358 AA;

W64217 Length: 358 April 26, 2000 08:15 Type: P Check: 6188

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTQVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDL LCSQPTDGEQ ALEICDALAR SGAVDVIWVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLAGNLKQ SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENNVGSETRV
 251 KVVKNKIAAP FKQAEFQILY DEGINFYGEL VDLGVKELI EKAGAWYSYK
 301 GEKAGOGKAN ATAWLKDNP TAKEIEKKVR ELLSNPNST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64218 standard; Protein: 358 AA.
 AC W64218;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 13.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-Al.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 Tobin MB;
 WPI: 98-427565/36.
 DR Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a wild-type recA protein (designated
 CC new Minshall), from an example of the present invention.
 SQ Sequence 358 AA;

DR N-PSDB; V44290.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see W64213), from an example of the present invention.
 SQ Sequence 358 AA;

W64218 Length: 358 April 26, 2000 08:15 Type: P Check: 6188

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTQVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDL LCSQPTDGEQ ALEICDALAR SGAVDVIWVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLAGNLKQ SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENNVGSETRV
 251 KVVKNKIAAP FKQAEFQILY DEGINFYGEL VDLGVKELI EKAGAWYSYK
 301 GEKAGOGKAN ATAWLKDNP TAKEIEKKVR ELLSNPNST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64213 standard; Protein: 358 AA.
 AC W64213;
 DT 28-APR-1999 (first entry)
 DE New Minshall recA protein.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive sequence recombination; evolution.
 OS Escherichia coli.
 PN WO9831837-Al.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 Tobin MB;
 WPI: 98-427565/36.
 N-PSDB; V44285.
 DR Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a wild-type recA protein (designated
 CC new Minshall), from an example of the present invention.
 SQ Sequence 358 AA;

W64213 Length: 358 April 26, 2000 08:15 Type: P Check: 6469

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTQVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDL LCSQPTDGEQ ALEICDALAR SGAVDVIWVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLAGNLKQ SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENNVGSETRV

251 KVVKNKIRAP FKQAEFQILY GEGINFYGEL VDLGVKEKLI EKAGAWYSYK
 301 GEKIGOGKAN ATAWLKDNPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG
 351 VAETNEDF

!!AA_SEQUENCE 1.0

ID W64214 standard; Protein: 358 AA.

AC W64214;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant reca protein clone 2.

KW Escherichia coli; reca protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

Escherichia coli.

Synthetic.

WO9831837-A1.

23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshull J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI; 98-427565/36.

DR N-PSDB; V44286.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of

CC recombination and selection/screening for evolution of whole cells

CC and organisms toward acquisition of desired properties, e.g.

CC enhanced recombination, genome copy number, and capacity for

CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC reca protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64214 Length: 358 April 26, 2000 08:15 Type: P Check: 7100 ..

1 MTGVRWAIDE NKQALRTAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTLQVIAAAQ REGKTCAFID

101 AEHALDPIYA RKLGVDIDNL LCSQPTGEG ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKPYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVVKNKIRAP FKQAEFQILY GEGINFYGEL VDLGVKEKLI EKAGAWYSYK

301 GEKIGOGKAN ATAWLKDNPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDF

! FINDPATTERNS on geneseqp:* allowing 0 mismatches

```

! 1 (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)PMGRIVEIY
W64215 ck: 6091 len: 358 ! Hyperrecombinogenic variant reca protein cl
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
46: MDVET (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
ISTGSLSLDIALGAGGLPMGRIVEIY

W64216 ck: 5676 len: 358 ! Hyperrecombinogenic variant reca protein cl
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
46: MDVET (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
ISTGSLSLDIALGAGGLPMGRIVEIY

W64217 ck: 6188 len: 358 ! Hyperrecombinogenic variant reca protein cl
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
46: MDVET (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
ISTGSLSLDIALGAGGLPMGRIVEIY

W64218 ck: 6188 len: 358 ! Hyperrecombinogenic variant reca protein cl
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
46: MDVET (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
ISTGSLSLDIALGAGGLPMGRIVEIY

W64213 ck: 6459 len: 358 ! New minshall reca protein. Evolution of who
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
46: MDVET (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
ISTGSLSLDIALGAGGLPMGRIVEIY

W64214 ck: 7100 len: 358 ! Hyperrecombinogenic variant reca protein cl
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
46: MDVET (I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
ISTGSLSLDIALGAGGLPMGRIVEIY

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Databases searched:

GenesEq, Release 36.3, Released on 8Jul1999, Formatted on 9Jul1999

Total finds: 6
Total length: 23,686,106
Total sequences: 188,963
CPU time: 04:02.75

!!AA_SEQUENCE 1.0

ID W64215 standard; Protein: 358 AA.

AC W64215;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant reca protein clone 4.

KW Escherichia coli: reca protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN WO9831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXI-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI: 98-427565/36.

DR N-PSDB; V44287.

PT Evolution of whole cells and organisms - by recursive DNA sequence
PT recombination in cells to evolve cells having acquired desired
PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of
CC recombination and selection/screening for evolution of whole cells
CC and organisms toward acquisition of desired properties, e.g. for
CC enhanced recombinogenicity, genome copy number, and capacity for
CC expression and/or secretion of proteins and secondary metabolites.
CC The present sequence represents a hyperrecombinogenic variant of a
CC reca protein (see w64213), from an example of the present invention.
SQ Sequence 358 AA;

W64215 Length: 358 April 26, 2000 08:16 Type: P Check: 6091

1 MTGVNNAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRC MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTQVIAAAQ REGKTCAFID

101 AEHALDPIYA RKLGVDDIDL LCSQPDTEGEQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLKL SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVVKNKIRAP FKQAEFOILY GEGINFYGEL VDLGVKEKLI EKAGAWISVK

301 GKVQGGKAN ATAWLKNDPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDE

!!AA_SEQUENCE 1.0

ID W64216 standard; Protein: 358 AA.

AC W64216;

DT 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant reca protein clone 5.

KW Escherichia coli: reca protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PN WO9831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXI-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI: 98-427565/36.

DR N-PSDB; V44288.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of

CC recombination and selection/screening for evolution of whole cells

CC and organisms toward acquisition of desired properties, e.g.

CC enhanced recombinogenicity, genome copy number, and capacity for

CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC reca protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64216 Length: 358 April 26, 2000 08:16 Type: P Check: 5676

1 MTGVNNAIDE NKQKALAAAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTQVIAAAQ REGKTCAFID

101 AEHALDPIYA RKLGVDDIDL LCSQPDTEGEQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLKL SNTLLIFINQ

201 IRMKIGVMFG NPETTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVKYKNTAAP FKAQEFQILY DGINFYGEL VDLGVKKEKLI EKAGAWYSYK
 301 GERAGOGKAN AAWLKGNP TAKEIEKKVR ELLLSNPST PDSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64217 standard; Protein; 358 AA.
 AC W64217;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 6.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-A1.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB;
 DR WPI; 98-427565/36.
 DR N-PSDB; V44289.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see w64213), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64217 Length: 358 April 26, 2000 08:16 Type: P Check: 6188
 1 MTGVKMAIDE NKQKALAAAL GQIEKQFGK SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTQVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDL LCSQPDTEQ ALEICDALAR SGAVDVIVVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV
 251 KVKYKNTAAP FKAQEFQILY DGINFYGEL VDLGVKKEKLI EKAGAWYSYK
 301 GERAGOGKAN ATAWLKDNP TAKEIEKKVR ELLLSNPST PDSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64218 standard; Protein; 358 AA.
 AC W64218;
 DT 28-APR-1999 (first entry)
 DE Hyperrecombinogenic variant recA protein clone 13.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 OS Escherichia coli.
 OS Synthetic.
 PN WO9831837-A1.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB;
 DR WPI; 98-427565/36.

DR N-PSDB; V44290.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a hyperrecombinogenic variant of a
 CC recA protein (see w64213), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64218 Length: 358 April 26, 2000 08:16 Type: P Check: 6188

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGK SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTQVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDL LCSQPDTEQ ALEICDALAR SGAVDVIVVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV
 251 KVKYKNTAAP FKAQEFQILY DGINFYGEL VDLGVKKEKLI EKAGAWYSYK
 301 GERAGOGKAN ATAWLKDNP TAKEIEKKVR ELLLSNPST PDSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0
 ID W64213 standard; Protein; 358 AA.

AC W64213;
 DT 28-APR-1999 (first entry)
 DE New Minshall recA protein.
 KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;
 KW recursive recombination; evolution.
 OS Escherichia coli.
 PN WO9831837-A1.
 PD 23-JUL-1998.
 PF 16-JAN-1998; U00852.
 PR 17-JAN-1997; US-035054.
 PA (MAXY-) MAXYGEN INC.
 PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,
 PI Tobin MB; 98-427565/36.
 DR N-PSDB; V44285.
 PT Evolution of whole cells and organisms - by recursive DNA sequence
 PT recombination in cells to evolve cells having acquired desired
 PT function
 PS Example 1; Fig 13; 125pp; English.
 CC The present invention provides methods employing iterative cycles of
 CC recombination and selection/screening for evolution of whole cells
 CC and organisms toward acquisition of desired properties, e.g.
 CC enhanced recombinogenicity, genome copy number, and capacity for
 CC expression and/or secretion of proteins and secondary metabolites.
 CC The present sequence represents a wild-type recA protein (designated
 CC new Minshall), from an example of the present invention.
 CC Sequence 358 AA;
 SQ

W64213 Length: 358 April 26, 2000 08:16 Type: P Check: 6469

1 MTGVKMAIDE NKQKALAAAL GQIEKQFGK SIMRLGEDRS MDVETISTGS
 51 LSLDIALGAG GLPMGRIVEI YGPSSGKTT LTQVIAAAQ REGKTCAFID
 101 AEHALDPIYA RKLGVDDIDL LCSQPDTEQ ALEICDALAR SGAVDVIVVE
 151 SVAALTPKAE IEGEIGDSHM GLAARMMSQA MRKLGNLQK SNTLLIFINQ
 201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVKEG ENVVGSETRV

251 KVVKNKIAAP FKQAEFQILY GEGINFYGEL VDLGVKKEKLI EKAGAWTSYK
 301 GEKIGQGRAN ATAWLKDNPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG
 351 VAETNEDE

!!AA_SEQUENCE 1.0

ID W64214 standard; Protein; 358 AA.

AC W64214;

DE 28-APR-1999 (first entry)

DE Hyperrecombinogenic variant recA protein clone 2.

KW Escherichia coli; recA protein; hyperrecombinogenic variant; Minshall;

KW recursive sequence recombination; evolution.

OS Escherichia coli.

OS Synthetic.

PA W09831837-A1.

PD 23-JUL-1998.

PF 16-JAN-1998; U00852.

PR 17-JAN-1997; US-035054.

PA (MAXY-) MAXYGEN INC.

PI Delcardayre SB, Minshall J, Ness JE, Patten P, Stemmer WPC,

PI Tobin MB;

DR WPI; 98-427565/36.

DR N-PSDB; V44286.

PT Evolution of whole cells and organisms - by recursive DNA sequence

PT recombination in cells to evolve cells having acquired desired

PT function

PS Example 1; Fig 13; 125pp; English.

CC The present invention provides methods employing iterative cycles of

CC recombination and selection/screening for evolution of whole cells

CC and organisms toward acquisition of desired properties, e.g.

CC enhanced recombination, genome copy number, and capacity for

CC expression and/or secretion of proteins and secondary metabolites.

CC The present sequence represents a hyperrecombinogenic variant of a

CC recA protein (see w64213), from an example of the present invention.

SQ Sequence 358 AA;

W64214 Length: 358 April 26, 2000 08:16 Type: P Check: 7100 ..

1 MTGVKMAIDE NKQALRTAL GQIEKQFGKG SIMRLGEDRS MDVETISTGS

51 LSLDIALGAG GLPMGRIVEI YGPESGKTT LTIQVIAAAQ REGKTCAFID

101 AEHALDPIYA RKLGVIDIDL LCSQPDTEQ ALEICDALAR SGAVDVIVVE

151 SVAALTPKAE IEGEIGDSHM GLAARMSQA MRKLGNLQK SNTLLIFINQ

201 IRMKIGVMFG NPETTTGGNA LKFYASVRLD IRRIGAVREG ENVVGSETRV

251 KVVKNKIAAP FKQAEFQILY GEGINFYGEL VDLGVKKEKLI EKAGAWTSYK

301 GEKIGQGRAN ATAWLKDNPE TAKEIEKKVR ELLLSNPNST PDFSVDDSEG

351 VAETNEDE


```

! FINDPATTERNS on swp:* allowing 0 mismatches
!
1 1 IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)
    RECA_ECOLI ck: 8674 len: 352 | P03017 escherichia coli, and shigella flexner
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
40: MDVET

1 RECA_ENTAG ck: 7629 len: 354 | P33037 enterobacter agglomerans. reca prote
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

1 RECA_PROVU ck: 9127 len: 325 | P26346 proteus vulgaris. reca protein. 12/1
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

1 RECA_SERMA ck: 5093 len: 354 | P17479 serratia marcescens. reca protein. 1
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

1 RECA_SHISO ck: 8506 len: 352 | Q9zff6 shigella sonnei. reca protein. 12/19
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
40: MDVET

1 RECA_XENBV ck: 6641 len: 358 | P96185 xenorhabdus bovienii. reca protein.
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

1 RECA_YERPE ck: 8556 len: 356 | P37858 yersinia pestis. reca protein. 12/19
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

1 Q9X5P5 ck: 4576 len: 358 | Q9X5P5 xenorhabdus nematophilus. reca prote
    IST(G,F,K,Y,R,W)SLSDIAL(G,F,K,Y,R,W)(A,F,K,Y,R,W)(G,F,K,Y,R,W)(G,F,K,Y,R,W)(G,
    IST(G)SLSDIAL(G)(A)(G)(G)LPM(G)RIVEIY
    ISTGSLSDIALGAGGLPMGRIVEIY GPESS
41: MDVET

Databases searched:
SWISS-PROT, Release 38.1, Released on 20Nov1999, Formatted on 28Dec1999
SPRMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 8
Total length: 99,198,988
Total sequences: 308,107
CPU time: 07:02.03

! IAA_SEQUENCE 1.0
ID RECA_ECOLI STANDARD;
AC P03017; P26347; P78213;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA OR LEXB OR UMUB OR RECH OR RNMB OR TIF OR ZAB.
OS Escherichia coli, and Shigella flexneri.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
[1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RC SPECIES=E.COLI;
RX MEDLINE; 80145618.
RA HORII T., OGAWA T., OGAWA H.;
RT "Organization of the reca gene of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:313-317(1980).
[2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-2.
RC SPECIES=E.COLI;
RX MEDLINE; 80234673.
RA SANCAR A., STACHELEK C., KONIGSBERG W., RUPP W.D.;
RT "Sequences of the reca gene and protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:2611-2615(1980).
[3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI, AND S.FLEXNERI; STRAIN=B/R;
RX MEDLINE; 91109725.
RA ZHAO X.J., MCENTEE K.;
RT "DNA sequence analysis of the reca genes from Proteus vulgaris,
RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Gen. Genet. 222:369-376(1990).
[4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI; STRAIN=K12 / MG1655;
RX MEDLINE; 97426617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI; STRAIN=K12;
RX MEDLINE; 97349980.
RA YAMAMOTO Y., AIBA H., BABA T., HAYASHI K., INADA T., ISONO K.,
RA ITOH T., KIMURA S., KITAGAWA M., MAKINO K., MIKI T., MITSUHASHI N.,
RA MIZOBUCHI K., MORI H., NAKADE S., NAKAMURA Y., NASHIMOTO H.,
RA OSHIMA T., OYAWA S., SAITO N., SAMPEI G., SATOH Y., SIVASUNDARAM S.,
RA TAGAMI H., TAKAHASHI H., TAKEDA J., TAKEMOTO K., UEHARA K., WADA C.,
RA YAMAGATA S., HORIUCHI T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
[6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC SPECIES=E.COLI;
RX MEDLINE; 92114994.
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RT "The structure of the E. coli reca protein monomer and polymer.";
RL Nature 355:318-325(1992).
[7]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 97185905.
RA YU X., EGELMAN E.H.;
RT "The RecA hexamer is a structural homologue of ring helicases.";
RL Nat. Struct. Biol. 4:101-104(1997).
[8]
RP ERRATUM.
RC SPECIES=E.COLI;
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RL Nature 355:567-567(1992).
[9]

```

RP STRUCTURE OF ATP-BINDING FOLD.
 RC SPECIES=E.COLI:
 RX MEDLINE: 92115005.
 RA STORY R.M., STEITZ T.A.;
 RL "Structure of the reca protein-ADP complex.";
 RL Nature 355:374-376(1992).
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -!- INDUCTION: IN RESPONSE TO LOW TEMPERATURE. SENSITIVE TO
 CC TEMPERATURE THROUGH CHANGES IN THE LINKING NUMBER OF THE DNA.
 CC -!- DATABASE: NAME=E.COLI reca Web page;
 CC WWW="http://monera.ncl.ac.uk:80/protein/final/reca.htm".
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: V00328; CAA23618.1;
 CC EMBL: X55553; CAB56806.1;
 CC EMBL: AE000354; AAC75741.1;
 CC EMBL: D90892; CAB22490.1;
 CC PIR: A03548; ROECA.
 CC PIR: S11931; S11931.
 CC PDB: 1REA; 31-OCT-93.
 CC PDB: 2REB; 31-OCT-93.
 CC PDB: 2REC; 01-APR-97.
 CC PDB: 1AA3; 23-JUL-97.
 CC SWISS-2DPAGE; P03017; COLI.
 CC ECO2DBASE; C039.3; 6TH EDITION.
 CC ECOGENE; EG10823; RECA.
 CC PROSITE; PS00321; RECA.
 CC PFM; PF00154; reca; 1.
 CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
 CC 3D-structure.
 CC INIT MET 0 0
 CC NP_BIND 66 73
 CC CONFLICT 112 112
 CC TURN 4 4
 CC HELIX 5 21
 CC TURN 23 25
 CC TURN 29 30
 CC STRAND 39 40
 CC HELIX 45 50
 CC TURN 51 51
 CC STRAND 56 57
 CC TURN 58 59
 CC STRAND 61 65
 CC TURN 68 69
 CC HELIX 72 85
 CC TURN 86 87
 CC STRAND 90 94
 CC HELIX 101 106
 CC TURN 107 108
 CC HELIX 111 113
 CC STRAND 115 117
 CC HELIX 122 135
 CC STRAND 140 144
 CC HELIX 146 148
 CC HELIX 152 155
 CC HELIX 166 185
 CC TURN 186 186
 CC TURN 188 193
 CC STRAND 213 218
 CC HELIX 221 223

FT TURN 234 235
 FT STRAND 236 249
 FT STRAND 257 263
 FT TURN 264 266
 FT STRAND 267 268
 FT HELIX 270 280
 FT TURN 281 282
 FT STRAND 285 287
 FT TURN 288 289
 FT STRAND 290 293
 FT TURN 294 295
 FT STRAND 296 300
 FT HELIX 301 311
 FT HELIX 313 327
 SQ SEQUENCE 352 AA; 37842 MW; A6DE5451 CRC32;
 RECA_ECOLI Length: 352 April 26, 2000 08:19 Type: P Check: 8674
 1 AIDENKQKAL AALGQIEKQ FGKGSIMRLG EDRSMDVETI STGSLSLDIA
 51 LGAGGLPWGR IVEIYGPESS GKTTLTLQVI AAQREGKTC AFIDAEHALD
 101 PYARKLQVD IDNLLSQPD TGEQALEICD ALARSGAVDV IVDVSAALT
 151 PKAEIEGEIG DSHMGLAARM MSQAMRKLAG NLKQSNLTLLI FINQIRMKIG
 201 VMFGNPEITT GGNALKFYAS VRLDIRRIGA VKEGENVYGS ETRVYVYKVK
 251 IAAPFKQAEF QILYGEINF YGELVDLGVK EKLIKAGAW YSYKGEKIGQ
 301 GKANATAWLK DNPETAKEIE KKYRELLSN PNSTPDFSVD DSEGVATNE
 351 DF
 !!AA_SEQUENCE 1.0
 ID RECA_ENTAG STANDARD; PRT; 354 AA.
 AC P33037;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Enterobacter agglomerans.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Pantoea.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA RAPPOLD C.S.J., KLINGMUELLER W.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
 CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
 CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
 CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
 CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
 CC CLEAVAGE.
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L03291; AAA91766.1;
 CC PIR: S31481; S31481.
 CC HSP: P03017; 2REB.
 CC PROSITE: PS00321; RECA; 1.
 CC PFM: PF00154; reca; 1.
 CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 CC NP_BIND 67 74
 CC SEQUENCE 354 AA; 37898 MW; 629E9B60 CRC32;
 SQ

RECA_ENTAG Length: 354 April 26, 2000 08:19 Type: P Check: 7629

1 MAIDENKQKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLV DIDNLLCSOP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPRAIEGEI GDSHMGGLAAR MMSQAMRKL GNKNANTLL IFINQIRMKI
201 GVMFGNPETT TGNALKFYA SVRLDIRRG AIKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FQILYEGIN INGLIDLGV KHKLIKAGA WYSYNGEKIG
301 QGRANACNFL KENPKVAEL DKLRDMLLS GTGELSVATT AEDADDNMET
351 SEEF

!!AA_SEQUENCE 1.0
ID RECA_PROVU STANDARD; PRT; 325 AA.
AC P26346;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91109725.
RA ZHAO X., MCENTEE K.;
RT "DNA sequence analysis of the recA genes from Proteus vulgaris,
RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Gen. Genet. 232:369-376(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE [ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X5555; ; NOT_ANNOTATED_CDS.
CC DR HSSP; P03017; 2REB.
CC DR PROSITE; PS00321; RECA; 1.
CC DR PFAM; PF00154; recA; 1.
CC KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SQ SEQUENCE 325 AA; 34790 MW; D46C9851 ORC32;
RECA_PROVU Length: 325 April 26, 2000 08:19 Type: P Check: 9127

1 MAIDENKQKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLV DIDNLLCSOP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPRAIEGEI GDSHMGGLAAR MMSQAMRKL GNKNANTLL IFINQIRMKI
201 GVMFGNPETT TGNALKFYA SVRLDIRRG AIKGDGVVVG SETRVKVKVN

251 KVAAPFKQAE FQILYEGIN INGLVDLGV KHKLIKAGA WYSYNGDKIG
301 QGRANACNFL KENSLVKETK NFNGC

!!AA_SEQUENCE 1.0
ID RECA_SERMA STANDARD; PRT; 354 AA.
AC P17479;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-SM6;
RX MEDLINE; 90094239.
RA BALL T.K., WASMUTH C.R., BRAUNAGEL S.C., BENEDIK M.J.;
RT "Expression of Serratia marcescens extracellular proteins requires
RT recA.";
RL J. Bacteriol. 172:342-349(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M22935; AAA26567.1; -.
CC DR HSSP; P03017; 2REB.
CC DR PROSITE; PS00321; RECA; 1.
CC DR PFAM; PF00154; recA; 1.
CC KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SQ SEQUENCE 354 AA; 37909 MW; 2BC62FDE CRC32;
RECA_SERMA Length: 354 April 26, 2000 08:19 Type: P Check: 5093

1 MAIDENKQKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLV DIDNLLCSOP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPRAIEGEI GDSHMGGLAAR MMSQAMRKL GNKNANTLL IFINQIRMKI
201 GVMFGNPETT TGNALKFYA SVRLDIRRG AIKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FQILYEGIN INGLVDLGV KHKLIKAGA WYSYNGEKIG
301 QGRANACNFL KENPAIAEL DKLRDMLLS SGGELVAASG DDFEDDEAET

!!AA_SEQUENCE 1.0
ID RECA_SHISO STANDARD; PRT; 352 AA.
AC Q9ZFP6;
DT 15-DEC-1999 (Rel. 39, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.

OS Shigella sonnei.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Shigella.
 RL [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-KN1H104S;
 RA PARK Y.C., SHIN H.J., KIM Y.C.;
 RT "Cloning and nucleotide sequence of the recA gene from Shigella sonnei KN1H104S";
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RL
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL: AF101227; AAC72856.1; -
 DR PROSITE: PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT INIT_MET 0 BY SIMILARITY.
 FT NP_BIND 66 73 ATP (POTENTIAL).
 FT SEQUENCE 352 AA; 37799 MW; ADB29D96 CRC32;
 SQ
 RECA_SHISO Length: 352 April 26, 2000 08:19 Type: P Check: 8506

1 AIDENKQKAL AALAQIEKQ FGKGSIMRLG EDRSMDEVETI STGSLSLDIA
 51 LGAGGLPMGR IVEIYGPRESS GKTTLTQVI AALAQEGKTC AFIDAHAHALD
 101 PIYARKLGVD IDNLLCSQPD TGSQALEICD ALARSGAVDV IVDVSAALT
 151 PKAEIEGEGT DSHGLAARM MSQAMRKLKAG NLKQSNLLI FINQIRMKIG
 201 VMFGNPETTT GGNALKFYAS VRLDIRRIGA VKEGENVVGES ETRVKVVKNK
 251 IAAPFKQAEF QILYEGGINF YGELVDLGVK EXLIEKAGAW YSYKGEKIGQ
 301 GKANATAWLK DNPETAKEIE KKVRELLSN PNSTPDFSV DSEGVVAETNE
 351 DF

AA SEQUENCE 1.0
 ID RECA_XENBV STANDARD; PRT; 358 AA.
 AC P96185;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1999 (Rel. 39, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Xenorhabdus bovienii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Xenorhabdus.
 RL [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-T228/1;
 RA PINYON R.A., ORMSBY R., RALSTON H., THOMAS C.J.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL: AF101227; AAC72856.1; -
 DR PROSITE: PS00321; RECA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT INIT_MET 0 BY SIMILARITY.
 FT NP_BIND 66 73 ATP (POTENTIAL).
 FT SEQUENCE 352 AA; 37799 MW; ADB29D96 CRC32;
 SQ

CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL: U87924; AAD12585.1; -
 DR HSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 DR PFAM: PF00154; recA; 1.
 KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
 FT NP_BIND 67 74 ATP (POTENTIAL).
 FT SEQUENCE 358 AA; 38487 MW; 3587853C CRC32;
 SQ
 RECA_XENBV Length: 358 April 26, 2000 08:19 Type: P Check: 6641

1 MANDENKQKA LAALQIEK QFGKGSIMRL GENRSMOVET ISTGSLSLDI
 51 ALGAGGLPMG RIVEIYGPES SGKTTITLQV IASAQREGKT CAFIDAHAHAL
 101 DPVYAKKLGV DIDNLLCSQP DTGEQALEIC DALSRSGAVD VIVDVSVAAL
 151 TPKAIEGEI GDHMGGLAAR MMSQAMRKLK GNLKNSNTLL IFINQIRMKI
 201 GVFMGNPETT TGNALKFYA SVRLDIRRTG SVKNGDEVVG SETRVKVVKN
 251 KIAAPFKQAE FQILYEGGIN TFGELVDLGV KHKMVERAGA WYSVNGDKIG
 301 QOKANATYIL KEHPEVSAEL DKKLRELLLN NTGFFSSAVS DYVADYEDNG
 351 EVKNEEF

AA SEQUENCE 1.0
 ID RECA_YERPE STANDARD; PRT; 356 AA.
 AC P37858;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE RECA PROTEIN.
 GN RECA.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 RL [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN-231;
 RA KRYUKOV V.M., SUCHKOV I.Y., SAZYKIN I.S., MISHANKIN B.N.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
 CC
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 CC
 CC EMBL: X75336; CAA53084.1; -
 DR PIR: S37586; S37586.
 DR HSP: P03017; 2REB.
 DR PROSITE: PS00321; RECA; 1.
 DR PFAM: PF00154; recA; 1.
 DR

KW DNA damage: DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (BY SIMILARITY).
SQ SEQUENCE 356 AA; 37912 MW; 60B356BF CRC32;

RECA_YERPE Length: 356 April 26, 2000 08:19 Type: P Check: 8556 ..

1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPEP SGKTTLTQV IAAAQREGT CAFIDAEHAL
101 DPIYAKKLGV DIDNLLCSQP DTGEQALEIC DALTRSGAVD VIIVDSVAAL
151 TPKAEIEGEI GDSHMGAAAR MMSQAMRKLA GNKKNANTLL IFINQIRMKI
201 GVMFGNPETP TGGNALKEFYA SVRLDIRRG AVKDGDDVVG SETRVKVKVN
251 KIAAPFKQAE FQILYEGIN INGELVDLGV KKLIEKAGA WYSYVGDKIG
301 QOKANASNYL KENPANAEL DKKLREMLN GNGEOPVAA ATAEFADGAD
351 ETVNEEF

!!AA_SEQUENCE 1.0

ID Q9XSP5 PRELIMINARY; PRT; 358 AA.

AC Q9XSP5;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE RECA PROTEIN.

GN RECA.

OS Xenorhabdus nematophilus.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Xenorhabdus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AN6;

RA HEW F.H., THOMAS C.J.;

RT "Analysis of the Xenorhabdus nematophilus AN6 recA gene sequence.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE

CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF

CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT

CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS

CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC

CC CLEAVAGE.

EMBL; AF127333; AAD32599.1; ..

DR PROSITE; PS00321; RECA; 1.

KW DNA damage: DNA recombination; SOS response; ATP-binding; DNA-binding.

SQ SEQUENCE 358 AA; 38586 MW; 51984C91 CRC32;

Q9XSP5 Length: 358 April 26, 2000 08:19 Type: P Check: 4576 ..

1 MANDENKOKA LAAALGQIEK QFGKGSIMRL GENRSMDVET ISTGSLSLDI

51 ALGAGGLPMG RIVEIYGPEP SGKTTLTQV IAAAQREGT CAFIDAEHAL

101 DVIYAKKLGV DIDNLLCSQP DTGEQALEIC DALSRGAVD VIIVDSVAAL

151 TPKAEIEGEI GDSHMGAAAR MMSQAMRKLA GNKKNANTLL IFINQIRMKI

201 GVMFGNPETP PGGNALKEFYA SVRLDIRRG SVKNGDEVVG SETRVKVKVN

251 KVAAPFKQAE FQILYEGIN TLGELIDLV KHKWEEKAGA WYSYNGDKIG

301 QOKANATIYL KEHPETAEL NKKLRDLLH NTGDFSSAAS DYVTYEDNT

351 EEVNEEF

WQSEH (TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Apr 25 12:28:13 2000; MasPar time 43.83 seconds
Tabular output not generated.
41.128 Million cell updates/sec

Title: >seqimod
Description: (1-26) from 103.pep
Perfect Score: 140
Sequence: 1 ISTXSLSLDIALXXXLPMXRIIVEY 26

Scoring table: PAM 150
Gap 15

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl12
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 29.804; Variance 47.930; scale 0.622

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	140	100.0	358	2 Q9X5P5 RECA PROTEIN.	2.73e-14
2	124	88.6	363	2 Q9XBC1 RECA PROTEIN.	7.02e-11
3	122	87.1	339	2 Q9X5D8 RECA PROTEIN.	1.84e-10
4	115	82.1	131	2 O05556 RECA.	5.16e-09
5	113	80.7	347	2 Q92MS7 RECA PROTEIN.	1.37e-08
6	111	79.3	376	10 Q92UP2 RECA PROTEIN.	3.37e-08
7	108	77.1	119	2 Q31058 RECA (FRAGMENT).	1.36e-07
8	108	77.1	237	2 Q84402 RECA PROTEIN (FRAGMENT)	1.36e-07
9	108	77.1	237	2 Q84402 RECA PROTEIN (FRAGMENT)	1.36e-07
10	106	75.7	352	2 Q84556 RECA PROTEIN.	8.22e-06
11	99	70.7	237	2 Q86384 RECA PROTEIN (FRAGMENT)	4.33e-04
12	90	64.3	319	2 Q60057 RECA-LIKE PROTEIN.	1.46e-01
13	76	54.3	130	2 Q53854 NITRATE ABC TRANSPORT	3.22e-01
14	74	52.9	244	1 Q30150 CHALCONE SYNTHASE-LIKE	7.02e-01
15	72	51.4	389	10 Q43595 Y22 PROTEIN.	7.02e-01
16	72	51.4	389	10 Q43595 Y22 PROTEIN.	7.02e-01
17	67	47.9	701	2 Q51403 NA+/H+ ANTIPOTER (NAP	4.65e+00
18	66	47.1	541	4 Q94941 KIAA0860 PROTEIN.	6.72e+00
19	65	46.4	133	4 Q15292 HCAT-2B (FRAGMENT).	9.69e+00
20	65	46.4	173	6 Q02806 HIGH AFFINITY CATIONIC	9.69e+00

21	65	45.4	261	11 Q62971 RCAT2 (FRAGMENT).	9.68e+00
22	64	45.7	244	2 P73818 HYPOTHETICAL 27.5 KD P	1.39e+01
23	64	45.7	277	8 Q79317 HYPOTHETICAL 31.7 KD P	1.39e+01
24	64	45.7	277	8 Q79334 HYPOTHETICAL 31.7 KD P	1.39e+01
25	64	45.7	277	8 Q79381 HYPOTHETICAL 31.7 KD P	1.39e+01
26	64	45.7	277	8 Q79543 HYPOTHETICAL 31.8 KD P	1.39e+01
27	64	45.7	277	8 Q79543 HYPOTHETICAL 31.8 KD P	1.39e+01
28	64	45.7	277	8 Q79543 HYPOTHETICAL 31.8 KD P	1.39e+01
29	64	45.7	277	8 Q79543 HYPOTHETICAL 31.8 KD P	1.39e+01
30	64	45.7	277	8 Q79543 HYPOTHETICAL 31.8 KD P	1.39e+01
31	64	45.7	279	8 Q79345 HYPOTHETICAL 32.0 KD P	1.39e+01
32	64	45.7	279	8 Q79345 HYPOTHETICAL 32.0 KD P	1.39e+01
33	64	45.7	279	8 Q79348 HYPOTHETICAL 32.0 KD P	1.39e+01
34	64	45.7	279	8 Q79541 HYPOTHETICAL 32.3 KD P	1.39e+01
35	64	45.7	279	8 Q79541 HYPOTHETICAL 32.3 KD P	1.39e+01
36	64	45.7	280	8 Q79343 HYPOTHETICAL 32.3 KD P	1.39e+01
37	64	45.7	291	8 Q79309 HYPOTHETICAL 32.5 KD P	1.39e+01
38	63	45.0	105	1 Q28815 HYPOTHETICAL 12.4 KD P	1.98e+01
39	63	45.0	225	5 Q96702 SODIUM PROTON ANTIPOTR	1.98e+01
40	63	45.0	329	6 Q28536 CATIONIC AMINO ACID TR	1.98e+01
41	63	45.0	406	1 Q54309 ALCOHOL DEHYDROGENASE.	1.98e+01
42	63	45.0	619	11 Q08812 CATIONIC AMINO ACID TR	1.98e+01
43	63	45.0	624	11 P70608 CATIONIC AMINO ACID TR	1.98e+01
44	63	45.0	628	11 Q921G1 ECOTROPIC MURINE RETRO	1.98e+01
45	62	44.3	328	11 Q60458 CATIONIC AMINO ACID TR	2.82e+01

ALIGNMENTS

RESULT 1
ID Q9X5P5 PRELIMINARY; PRT; 358 AA.
AC Q9X5P5;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Xenorhabdus nematophilus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ANG;
RA HEW F.H., THOMAS C.J.;
RT "Analysis of the Xenorhabdus nematophilus AN6 recA gene sequence.";
RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AF127333; AAD32599.1; -
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
SQ SEQUENCE 358 AA; 38586 MW; 51984C91 CRC32;

Query Match 100.0%; Score 140; DB 2; Length 358;
Best Local Similarity 76.9%; Pred. No. 2.73e-14;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTXSLSLDIALGAGGLPMGRIVEY 66
Qy 1 ISTXSLSLDIALXXXLPMXRIIVEY 26

RESULT 2
ID Q9XBC1 PRELIMINARY; PRT; 363 AA.
AC Q9XBC1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN.

GN RECA
OS Rhodopsuomonas palustris.
OC Bacteria; Proteobacteria; alpha subdivision; Bradyrhizobium group;
OC Rhodopsuomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NO. 7.
RX MEDLINE; 99303337.
RA DUMAY V., INUI M., YUKAWA H.;
RT "Molecular analysis of the recA gene and SOS box of the purple non-
RT sulfur bacterium Rhodopsuomonas palustris no. 7";
RL Microbiology 145:1275-1285(1999).
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC
DR EMBL; D84467; BAA78779.1; -.
DR PROSITE; PS00321; RECA; 1.
DR DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
KW SEQUENCE 363 AA; 38865 MW; 81D3B0ED CRC32;

Query Match 88.6%; Score 124; DB 2; Length 363;
Best Local Similarity 65.4%; Pred. No. 7.02e-11;
Matches 17; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 52 ISSGSLGDLTALGVGLPKRIVEY 77
ID Q9X5D8 PRELIMINARY; PRT; 339 AA.
AC Q9X5D8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; alpha subdivision; Zymomonas group;
OC Zymomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZM4;
RA LEE H.J., KANG H.S.;
RT "Sequence analysis of 43D2 fosmid clone of Zymomonas mobilis ZM4";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC
DR EMBL; AF124757; AAD29645.1; -.
DR PROSITE; PS00321; RECA; 1.
DR DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
KW SEQUENCE 339 AA; 36807 MW; 21492B84 CRC32;

Query Match 87.1%; Score 122; DB 2; Length 339;
Best Local Similarity 65.4%; Pred. No. 1.84e-10;
Matches 17; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 37 ISSGSLGDLTALGVGLPKRIVEY 62
ID Q9X5D8 PRELIMINARY; PRT; 131 AA.
AC Q9X5D8;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE RECA.
GN RECA.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC BADOCK K., CHURCHER C.M.;
RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RA BARRELL B.G., RAJANDREAM M.A.;
RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93188700.
RA EIGLMEIER K., HONORE N., WOODS S.A., CAUDRON B., COLE S.T.;
RT "Use of an ordered cosmid library to deduce the genomic organization
RT of Mycobacterium leprae";
RL Mol. Microbiol. 7:197-206(1993).
DR EMBL; Z94723; CAB08125.1; -.
DR HSSP; P03017; 2REB.
DR PFAM; PF00154; RECA; 1.
SQ SEQUENCE 131 AA; 13616 MW; 18ECEB05 CRC32;

Query Match 82.1%; Score 115; DB 2; Length 131;
Best Local Similarity 57.7%; Pred. No. 5.16e-09;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Db 41 IPTGSLDVALGIGLPRGIVEY 66
ID Q9ZMS7 PRELIMINARY; PRT; 347 AA.
AC Q9ZMS7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Helicobacter pylori J99.
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-J99;
RX MEDLINE; 99120557.
RA ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C.;
RA SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G.;
RA TUMMINO P.J., CARUSO A., URITA-NICKELSEN M., MILLS D.M., IVES C.;
RA GIBSON R., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
RA TRUST T.J.;
RT "Genomic-sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori";
RL Nature 397:176-180(1999).
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC
DR EMBL; AE001453; AAD05722.1; -.
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding;
KW DNA-binding.
SQ SEQUENCE 347 AA; 37623 MW; 7812DC30 CRC32;

Query Match 80.7%; Score 113; DB 2; Length 347;

Best Local Similarity 57.7%; Pred. No. 1.32e-08;
Matches 15; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 41 ISTGSLDLDLALGIGVPGKRIEY 66
||| |||:||||| :|: |||:|||||
QY 1 ISTXSLDLIALXXXXLPMXRIEY 26

RESULT 6
ID Q92UP2 PRELIMINARY; PRT; 376 AA.
AC Q92UP2;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN.
RECA.
Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
RA FRASER C.M., VENTER J.C.;
RT "Arabidopsis thaliana chromosome II BAC F3p11 genomic sequence.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEAX CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AC005917; AAD10148.1; -.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding;
KW DNA-binding.
SQ SEQUENCE 376 AA; 40269 MW; 6F0F9ECB CRC32;

Query Match 79.3%; Score 111; DB 10; Length 376;
Best Local Similarity 53.8%; Pred. No. 3.37e-08;
Matches 14; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 39 FTGSGFALDVALGIGVPGKRIEY 64
||| |||:||||| |||: |||:|||||
QY 1 ISTXSLDLIALXXXXLPMXRIEY 26

RESULT 7
ID Q31058 PRELIMINARY; PRT; 119 AA.
AC Q31058;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA (FRAGMENT).
RECA.
OS Rhodothermus marinus.
OC Bacteria; Cytophagales; Rhodothermus group; Rhodothermus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R-10;
RA THOROLFSDOTTIR E., THORBJARNARDOTTIR S.H., EGERTSSON G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026690; AAB82716.1; -.
DR HSP; P03017; 2REB.
DR PFAM; PF00154; RECA; 1.
FT NON-TER 119
SQ SEQUENCE 119 AA; 12218 MW; B2A066C9 CRC32;

Query Match 77.1%; Score 108; DB 2; Length 119;
Best Local Similarity 57.7%; Pred. No. 1.36e-07;
Matches 15; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 42 IPTGSLDALGIGVPGKRIEY 67
||| |||:||||| |||: |||:|||||
QY 1 ISTXSLDLIALXXXXLPMXRIEY 26

RESULT 8
ID Q86402 PRELIMINARY; PRT; 237 AA.
AC Q86402;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN (FRAGMENT).
RECA.
OS Neisseria perflava.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LCDC 85402;
RA SMITH N.H., DONOVAN G.M., CARPENTER A., SPRATT B.G.;
RT "Do sexual bacteria have species?";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEAX CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AJ223862; CAAL1593.1; -.
DR HSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; RECA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
KW NON-TER 1
FT NON-TER 237
SQ SEQUENCE 237 AA; 25463 MW; 28426969 CRC32;

Query Match 77.1%; Score 108; DB 2; Length 237;
Best Local Similarity 60.0%; Pred. No. 1.36e-07;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 1 STGSLGLDLALGIGVPGKRIEY 25
||| |||:||||| |||: |||:|||||
QY 2 STXSLDLIALXXXXLPMXRIEY 26

RESULT 9
ID Q88150 PRELIMINARY; PRT; 237 AA.
AC Q88150;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE RECA PROTEIN (FRAGMENT).
RECA.
OS Neisseria lactamica.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUC 7757, NCTC 10618, LCDC 80-111, LCDC 845;
RA SMITH N.H., DONOVAN G.M., CARPENTER A., SPRATT B.G.;
RT "Do sexual bacteria have species?";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA. THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEAX CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AJ223866; CAAL1597.1; -.
DR EMBL; AJ223863; CAAL1594.1; -.

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DR EMBL; AJ223864; CAAL1595.1; -
DR EMBL; AJ223865; CAAL1596.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 25464 MW; B67CDB68 CRC32;

Query Match 77.1%; Score 108; DB 2; Length 237;
Best Local Similarity 60.0%; Pred. No. 1.36e-07;
Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 1 STGSLGDLALGVGGLPRGRIVEIF 25
|||:||||:
QY 2 STXSLDLALXXXLPMXRIEY 26
|||:||||:

RESULT 10
ID O84656 PRELIMINARY; PRT; 352 AA.
O84656;
01-NOV-1998 (TREMBlrel. 08, Created)
01-NOV-1998 (TREMBlrel. 08, Last sequence update)
01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE RECA PROTEIN.
CN RECA.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX;
RA STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
RA MITCHELL W.P., OLINGER L., TATSOV R.L., ZHAO Q., KOONIN E.V.,
RA DAVIS R.W.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AE001335; AAC68827.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
DR PRINTS; PR00142; RECA.
KW Hypothetical protein; DNA damage; DNA recombination; SOS response;
KW ATP-binding; DNA-binding.
SQ SEQUENCE 352 AA; 37830 MW; D4B5CCD3 CRC32;

Query Match 75.7%; Score 106; DB 2; Length 352;
Best Local Similarity 53.8%; Pred. No. 3.42e-07;
Matches 14; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 41 IKTGALSLLALGIGGVKGRIVEIF 66
|||:||||:
QY 1 ISTXSLDLALXXXLPMXRIEY 26
|||:||||:

RESULT 11
ID O86384 PRELIMINARY; PRT; 237 AA.
O86384;
01-NOV-1998 (TREMBlrel. 08, Created)

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DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE RECA PROTEIN (FRAGMENT).
CN RECA.
OS Neisseria flava.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BANGOR 9;
RA SMITH N.H., DONOVAN G.M., CARPENTER A., SPRATT B.G.;
RA "Do sexual bacteria have species?";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; AJ223873; CAAL1604.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NON_TER 1
FT NON_TER 237
SQ SEQUENCE 237 AA; 25461 MW; 2A50CC00 CRC32;

Query Match 70.7%; Score 99; DB 2; Length 237;
Best Local Similarity 52.0%; Pred. No. 8.22e-06;
Matches 13; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 1 STGSLGVDLALGVGGLPRGRIVEIF 25
|||:||||:
QY 2 STXSLDLALXXXLPMXRIEY 26
|||:||||:

RESULT 12
ID Q60057 PRELIMINARY; PRT; 319 AA.
Q60057;
01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE RECA PROTEIN (FRAGMENT).
OS Unknown prokaryotic organism.
OC Bacteria; environmental samples.
RN [1]
RP SEQUENCE FROM N.A.
RA BORCHELLINI P., ANGULO J., DEVORET R., BERTOLOTI R.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
DR EMBL; U20900; AAA62510.1; -
DR HSSP; P03017; 2REB.
DR PROSITE; PS00321; RECA; 1.
DR PFAM; PF00154; reca; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding;
KW DNA-binding.
FT NON_TER 319
FT NON_TER 319
SQ SEQUENCE 319 AA; 34041 MW; 507C1D67 CRC32;

Query Match 64.3%; Score 90; DB 2; Length 319;
Best Local Similarity 44.0%; Pred. No. 4.33e-04;
Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Db 54 PSGSVKLDLALGVGGLPRGRIVEIF 78
|||:||||:
QY 2 STXSLDLALXXXLPMXRIEY 26
|||:||||:

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Search completed: Tue Apr 25 12:30:04 2000
Job time : 111 secs.

! FINDPATTERNS on swp:* allowing 0 mismatches

1 1 (I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)PMGRIVEIY

RECA_ECOLI ck: 8674 len: 352 1 P03017 escherichia coli, and shigella flexneri
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
40: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_ENTAG ck: 7629 len: 354 1 P33037 enterobacter agglomerans. reca protease
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_PROVU ck: 9127 len: 325 1 P36346 proteus vulgaris. reca protein. 12/1
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_SERMA ck: 5093 len: 354 1 P17479 serratia marcescens. reca protein. 1
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_SHISO ck: 8506 len: 352 1 Q92ff6 shigella sonnei. reca protein. 12/19
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
40: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_XENBV ck: 6641 len: 358 1 P96185 xenorhabdus bovienii. reca protein.
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

RECA_YERPE ck: 8556 len: 356 1 P37858 yersinia pestis. reca protein. 12/19
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

Q9X5P5 ck: 4576 len: 358 1 Q9x5p5 xenorhabdus nematophilus. reca prote
(I,W,Y,F,H)S(T,W,Y,F,H)G(S,W,Y,F,H)LSLDI(A,W,Y,F,H)LGAGG(L,W,Y,F,H)
(I)S(T)G(S)LSLDI(A)LGAGG(L)PMGRIVEIY
41: MDVET ISTGSLSLDIALGAGGLPMGRIVEIY

Databases searched:
SWISS-PROT, Release 38.1, Released on 20Nov1999, Formatted on 28Dec1999
SPTRMBL, Release 12.0, Released on 1Nov1999, Formatted on 27Dec1999

Total finds: 8
Total length: 99,198,988
Total sequences: 308,107
CPU time: 14:31:00

!!AA_SEQUENCE 1.0
ID RECA_ECOLI
AC P03017; P26347; P78213; PRT; 352 AA.

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
RECA OR LEXB OR UMUB OR RECH OR RNMB OR TIF OR ZAB.
Escherichia coli, and Shigella flexneri.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.
RC SPECIES=E.COLI;
RX MEDLINE: 80145618.
RA HORII T., OGAWA T., OGAWA H.;
RT "Organization of the reca gene of Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:313-317(1980).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-2.
RC SPECIES=E.COLI;
RX MEDLINE: 80234673.
RA SANCAR A., STACHELEK C., KONIGSBERG W., RUPP W.D.;
RT "Sequences of the reca gene and protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:2611-2615(1980).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI, AND S.FLEXNERI; STRAIN=B/R;
RX MEDLINE: 91109725.
RA ZHAO X.J., MCENTEE K.;
RT "DNA sequence analysis of the reca genes from Proteus vulgaris,
RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Gen. Genet. 222:369-376(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI; STRAIN=K12 / MG1655;
RX MEDLINE: 97428617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
RA MAU B., SHAO Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.COLI; STRAIN=K12;
RX MEDLINE: 97349980.
RA YAMAMOTO Y., AIBA H., BABA T., HAYASHI K., INADA T., ISONO K.,
RA ITOH T., KIMURA S., KITAGAWA M., MAKINO K., MIKI T., MITSUHASHI N.,
RA MIZOBUCHI K., MORI H., NAKADE S., NAKAMURA Y., NASHIMOTO H.,
RA OSHIMA T., OYAMA S., SAITO N., SAMPEI G., SATOH Y., SIVASUNDARAM S.,
RA TAGAMI H., TAKAHASHI H., TAKEDA J., TAKEMOTO K., UEHARA K., WADA C.,
RA YAMAGAWA S., HORTUCHI T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT K12 genome corresponding to 50.0-66.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:191-113(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC SPECIES=E.COLI;
RX MEDLINE: 92114994.
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RT "The structure of the E. coli reca protein monomer and polymer.";
RL Nature 355:318-325(1992).
RN [7]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE: 97185905.
RA YU X., EGELMAN E.H.;
RT "The RecA hexamer is a structural homologue of ring helicases.";
RL Nat. Struct. Biol. 4:101-104(1997).
RN [8]
RP ERRATUM.
RC SPECIES=E.COLI;
RA STORY R.M., WEBER I.T., STEITZ T.A.;
RL Nature 355:567-567(1992).
RN [9]

RP STRUCTURE OF ATP-BINDING FOLD.
RX SPECIES-E.COLI;
RC MEDLINE; 92115005.
RT STORY R.M., STEITZ T.A.;
RA "Structure of the recA protein-ADP complex.";
RL Nature 355:374-376(1992).
CC -|- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -|- INDUCTION: IN RESPONSE TO LOW TEMPERATURE. SENSITIVE TO
CC TEMPERATURE THROUGH CHANGES IN THE LINKING NUMBER OF THE DNA.
CC -|- DATABASE: NAME-E.coli recA Web page;
CC WWW="http://monera.ncl.ac.uk:80/protein/final/recA.htm".
CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; V00328; CAA23618.1; -;
CC EMBL; X55553; CAB56806.1; -;
CC EMBL; AE000354; AAC75741.1; -;
CC EMBL; D90892; CAB22490.1; -;
CC PIR; A03548; ROECA.
CC PIR; S11931; S11931.
CC PDB; 1REA; 31-OCT-93.
CC PDB; 2REB; 31-OCT-93.
CC PDB; 2REC; 01-APR-97.
CC PDB; 1AA3; 23-JUL-97.
CC SWISS-2DPAGE; P03017; COLI.
CC ECODBASE; C039.3; 6TH EDITION.
CC ECOGENE; EG10823; RECA.
CC PROSITE; PS00321; RECA; 1.
CC PFAM; PF00154; recA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding;
KW 3D-structure.
FT INIT MET 0 0
FT NP_BIND 66 73 ATP.
FT CONFLICT 112 112 D -> E (IN REF. 5).
FT TURN 4 4
FT HELIX 5 21
FT TURN 23 25
FT TURN 29 30
FT STRAND 39 40
FT HELIX 45 50
FT TURN 51 51
FT STRAND 56 57
FT TURN 58 59
FT STRAND 61 65
FT TURN 68 69
FT HELIX 72 85
FT TURN 86 87
FT STRAND 90 94
FT HELIX 101 106
FT TURN 107 108
FT HELIX 111 113
FT STRAND 115 117
FT HELIX 122 135
FT STRAND 140 144
FT HELIX 146 148
FT HELIX 152 155
FT HELIX 166 185
FT TURN 186 186
FT TURN 188 193
FT STRAND 213 218
FT HELIX 221 233

FT TURN 234 235
FT STRAND 236 249
FT STRAND 257 263
FT TURN 264 266
FT STRAND 267 268
FT HELIX 270 280
FT TURN 281 282
FT STRAND 285 287
FT TURN 288 289
FT STRAND 290 293
FT TURN 294 295
FT STRAND 296 300
FT HELIX 301 311
FT HELIX 313 327
SQ SEQUENCE 352 AA; 37842 MW; A6DE5451 CRC32;

RECA_ECOLI Length: 352 April 26, 2000 08:21 Type: P Check: 8674

1 AIDENKQKAL AALGQIEKQ FKGSMIRLG EDRSMVETI STGSLSLDIA
51 LGAGGLPMGR IVEIYGESS GKTTLTLOVI AAQREGKTC AFIDAHAHALD
101 PIYARKLQVD IDNLLCSQPD TGEQALEICD ALARSGAVDV IIVDSVAALT
151 PKAEIEGEIG DSHMGLAARM MSQAMRKLKAG NLKOSNTLLI FINQIRKKIG
201 VMFCNPETTT GGNALKFYAS VRLDIRRIGA VKEGENVVGS ETRVKVVKNK
251 IAAFPKQAEF QIILYGEINP YGELYDLGVK EKLIEKAGAW YSYKGEKIGQ
301 GKANATAWLK DNPETAKEIE KKVRELLLSN PNSTPDFSVD DSEGVAETNE
351 DF

11AA_SEQUENCE 1.0
ID RECA_ENTAG STANDARD; PRT; 354 AA.
AC P33037;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Enterobacter agglomerans.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pantoea.
RN [1]
RP SEQUENCE FROM N.A.
RA RAPPOLD C.S.J., KLINGMUELLER W.;
RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -|- SIMILARITY: BELONGS TO THE RECA FAMILY.
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CC -----
CC EMBL; L03291; AAA91766.1; -;
CC PIR; S31481; S31481.
CC HSSP; P03017; 2REB.
CC PROSITE; PS00321; RECA; 1.
CC PFAM; PF00154; recA; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (BY SIMILARITY).
SQ SEQUENCE 354 AA; 37898 MW; 629E3B60 CRC32;

RECA_ENTAG Length: 354 April 26, 2000 08:21 Type: P Check: 7629

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1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLGVDIDNLLCSQ DTGEQALEIC DALTRSGAVD VVIYDSVAAL
151 TPRAEIEGEI GDSHGLAAR MMSQAMRCLA GNKKNANTLL IFINQIRMKI
201 GVMFGNPETT TGGNALKFYA SVRLDIRRIG AIKEDGVVVG SETRVKVVKN
251 KIAAPFKQAE FOILYGEIN INGEIDLVG KHKLEKAGA WYSYNGEKIG
301 OGRANSCNYL KENPKVAEL DKLRDMLLS GTGELSVATT AEDADDNMET
351 SEEF

!!AA_SEQUENCE 1.0
ID RECA_PROVU STANDARD; PRT; 325 AA.
AC P26346;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91109725.
RA "DNA sequence analysis of the recA genes from Proteus vulgaris,
RT Erwinia carotovora, Shigella flexneri and Escherichia coli B/r.";
RL Mol. Genet. 222:369-376(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC -----
CC EMBL: X55555; -; NOT_ANNOTATED_CDS.
CC HSSP: P03017; 2REB.
CC PROSITE: PS00321; RECA; 1.
CC PFAM: PF00154; recA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SEQUENCE 325 AA; 34790 MW; D46C9851 CRC32;
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RECA_PROVU Length: 325 April 26, 2000 08:21 Type: P Check: 9127

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1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
101 DPIYAKKLGVDIDNLLCSQ DTGEQALEIC DALTRSGAVD VVIYDSVAAL
151 TPRAEIEGEI GDSHGLAAR MMSQAMRCLA GNKKNANTLL IFINQIRMKI
201 GVMFGNPETT TGGNALKFYA SVRLDIRRIG AIKEDGVVVG SETRVKVVKN
```

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251 KIAAPFKQAE FOILYGEIN INGEIDLVG KHKLEKAGA WYSYNGDKIG
301 OGRANACNLF KENSLVKETK NFNGC
```

```
!!AA_SEQUENCE 1.0
ID RECA_SERMA STANDARD; PRT; 354 AA.
AC P17479;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE RECA PROTEIN.
GN RECA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90094239.
RA BALL T.K., WASMUTH C.R., BRAUNAGEL S.C., BENEDIK M.J.;
RT "Expression of Serratia marcescens extracellular proteins requires
RL J. Bacteriol. 172:342-349(1990).
CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE
CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF
CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT
CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS
CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC
CC CLEAVAGE.
CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M22335; AAA26567.1; -
CC HSSP: P03017; 2REB.
CC PROSITE: PS00321; RECA; 1.
CC PFAM: PF00154; recA; 1.
CC DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
CC NP_BIND 67 74 ATP (BY SIMILARITY).
CC SEQUENCE 354 AA; 37909 MW; 2BC62FDE CRC32;
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RECA_SERMA Length: 354 April 26, 2000 08:21 Type: P Check: 5093

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1 MAIDENKOKA LAAALGQIEK QFGKGSIMRL GEDRSMDET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SGKTTTLQV IAAAREGKT CAFIDAEHAL
```

```
101 DPIYAKKLGVDIDNLLCSQ DTGEQALEIC DALTRSGAVD VVIYDSVAAL
```

```
151 TPRAEIEGEI GDSHGLAAR MMSQAMRCLA GNKKNANTLL IFINQIRMKI
```

```
201 GVMFGNPETT TGGNALKFYA SVRLDIRRIG AIKEDGVVVG SETRVKVVKN
```

```
251 KIAAPFKQAE FOILYGEIN INGEIDLVG KHKLEKAGA WYSYNGEKIG
```

```
301 OGRANACNLF KENPKVAEL DKLRDMLLS SGELVAAASG DDFEDDEAET
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351 SEQF
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!!AA_SEQUENCE 1.0
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ID RECA_SHISO STANDARD; PRT; 352 AA.
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AC Q92FF6;
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DT 15-DEC-1999 (Rel. 39, Created)
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DT 15-DEC-1999 (Rel. 39, Last sequence update)
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DT 15-DEC-1999 (Rel. 39, Last annotation update)
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DE RECA PROTEIN.
```

```
GN RECA.
```

[illegible]

KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NP_BIND 67 74 ATP (BY SIMILARITY).
SQ SEQUENCE 356 AA; 37912 MW; 60B356BF GRC32;

RECA_YERPE Length: 356 April 26, 2000 08:21 Type: P Check: 8556 ..

1 MAIDENKKA LAAALGQIEK QFGKGSIMRL GEDRSMDEVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SKTTLTLQV IAAQREGKT CAFIDAEHAL
101 DPIYAKKLG V DIDNLLCSQP DTGEQALEIC DALTRSGAVD VIVDSVAAL
151 TPKEIEGEI GDHMGGLAAR MMSQAMKLA GNKKNANTLL IFINQIRMKI
201 GVMEGNPETT TGGNALKFYA SVRLDIRRG AVKGDGVVVG SETRVKVKVN
251 KIAAPFKQAE FQILYGBGIN INGELYDLGV KKLIEKAGA WYSYGDKIG
301 QGKANASNYL KENPANAAEL DKKLREMLLN GNGEQPVAA ATAEFADGAD
351 ETNEEF

!!AA_SEQUENCE 1.0

ID Q9X5P5 PRELIMINARY; PRT; 358 AA.

AC Q9X5P5;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE RECA PROTEIN.

OS RECA.

OS xenorhabdus nematophilus.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Xenorhabdus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-AM6;

RA HEW F.H., THOMAS C.J.;

RT "Analysis of the Xenorhabdus nematophilus AN6 reca gene sequence."

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases

CC -!- FUNCTION: RECA PROTEIN CAN CATALYZE THE HYDROLYSIS OF ATP IN THE

CC PRESENCE OF SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF

CC SINGLE-STRANDED DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT

CC HYBRIDIZATION OF HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS

CC WITH LEXA CAUSING ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC

CC CLEAVAGE.

EMBL: AF127333; AAD32599.1; ..

DR PROSITE; PS00321; RECA; 1.

KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.

SQ SEQUENCE 358 AA; 38586 MW; 51984C91 GRC32;

Q9X5P5 Length: 358 April 26, 2000 08:21 Type: P Check: 4576 ..

1 MANDENKKA LAAALGQIEK QFGKGSIMRL GENRSMDEVET ISTGSLSLDI
51 ALGAGGLPMG RIVEIYGPE SKTTLTLQV IAAQREGKT CAFIDAEHAL
101 DPVYAKKLG V DIDNLLCSQP DTGEQALEIC DALTRSGAVD VIVDSVAAL
151 TPKEIEGEI GDHMGGLAAR MMSQAMKLA GNKKNANTLL IFINQIRMKI
201 GVMEGNPETP PGGNALKFYA SVRLDIRRG SVKNGDEVVG SETRVKVKVN
251 KVAAPFKQAE FQILYGBGIN TLGELIDLSV KHKMVEKAGA WYSYNGDKIG
301 QGKANATYYL KERPETAEL NKKLRDLLLH NTGDFSSAAS DYVTDYEDNT
351 EEVNNEEF

